

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 16, 2003, 18:10:03 : Search time 16 Seconds  
(without alignments)  
15.667 Million cell updates/sec

Title: US-09-780-612A-1

Perfect score: 35

Sequence: 1 GRGTP 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4210858 residues

Total number of hits satisfying chosen parameters: 37639

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCITUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	1	US-08-169-743-2
2	35	100.0	6	1	US-08-178-482-7
3	35	100.0	6	1	US-08-234-997-1
4	35	100.0	6	2	US-08-747-137-74
5	35	100.0	6	2	US-08-747-137-176
6	35	100.0	6	3	US-08-696-699-1
7	35	100.0	6	4	US-09-696-477-1
8	35	100.0	6	4	US-09-485-653-1
9	35	100.0	6	4	US-09-548-697A-2
10	35	100.0	6	5	PCT-US93-05640-45
11	31	88.6	6	1	US-07-720-222-46
12	31	88.6	6	1	US-07-780-790A-6
13	31	88.6	6	1	US-07-932-200-11
14	31	88.6	6	1	US-08-234-973-3
15	31	88.6	6	1	US-08-251-027-13
16	31	88.6	6	1	US-08-214-770-13
17	31	88.6	6	1	US-08-212-186A-2
18	31	88.6	6	1	US-08-169-743-4
19	31	88.6	6	1	US-08-262-315-1
20	31	88.6	6	1	US-08-425-238-7
21	31	88.6	6	1	US-08-178-482-6
22	31	88.6	6	1	US-08-264-759-3
23	31	88.6	6	1	US-08-445-745-49
24	31	88.6	6	1	US-08-608-697-1
25	31	88.6	6	1	US-08-596-116A-69
26	31	88.6	6	1	US-08-104-335-3
27	31	88.6	6	1	US-08-421-702A-4

28	31	88.6	6	1	US-08-482-106-16	Sequence 16, Appl
29	31	88.6	6	1	US-08-303-052A-4	Sequence 4, Appl
30	31	88.6	6	1	US-08-421-696A-4	Sequence 4, Appl
31	31	88.6	6	1	US-07-803-623H-12	Sequence 12, Appl
32	31	88.6	6	1	US-08-482-107B-3	Sequence 3, Appl
33	31	88.6	6	1	US-08-421-697A-4	Sequence 4, Appl
34	31	88.6	6	1	US-08-421-698A-4	Sequence 4, Appl
35	31	88.6	6	2	US-08-387-749-11	Sequence 11, Appl
36	31	88.6	6	2	US-08-520-535-15	Sequence 15, Appl
37	31	88.6	6	2	US-08-280-646-2	Sequence 2, Appl
38	31	88.6	6	2	US-08-445-193-2	Sequence 2, Appl
39	31	88.6	6	2	US-08-432-69A-2	Sequence 2, Appl
40	31	88.6	6	2	US-08-635-572-1	Sequence 1, Appl
41	31	88.6	6	2	US-08-806-064-12	Sequence 12, Appl
42	31	88.6	6	2	US-08-421-695A-4	Sequence 4, Appl
43	31	88.6	6	2	US-08-473-025-3	Sequence 3, Appl
44	31	88.6	6	2	US-08-447-810-2	Sequence 2, Appl
45	31	88.6	6	2	US-08-585-281-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-08-169-743-2  
: Sequence 2, Application US/08169743  
: Patent No. 5547936  
: GENERAL INFORMATION:  
: APPLICANT: RUOSLAHTI, ERKKI  
: APPLICANT: PIERSBACHER, MICHAEL D.  
: APPLICANT: GEHLEN, KURT R.  
: TITLE OF INVENTION: INHIBITION OF CELL MIGRATION WITH  
: TITLE OF INVENTION: SYNTHETIC PEPTIDES  
: NUMBER OF SEQUENCES: 6  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK  
: STREET: 444 SOUTH FLOWER STREET, SUITE 2000  
: CITY: LOS ANGELES  
: STATE: CALIFORNIA  
: COUNTRY: UNITED STATES  
: ZIP: 90071  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/169,743  
: FILING DATE:  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/773,106  
: FILING DATE: 08-OCT-1992  
: ATTORNEY/AGENT INFORMATION:  
: NAME: BROWN, THERESA A.  
: REGISTRATION NUMBER: 32,547  
: REFERENCE/DOCKET NUMBER: P419102  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 619-535-9601  
: TELEFAX: 619-535-8849  
: INFORMATION FOR SEQ ID NO: 2:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 6 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
US-08-169-743-2

Query Match 100.0%; Score 35; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGTP 6  
|||||

Db 1 GRGDT 6

## RESULT 2

US-08-178-482-7  
 : Sequence 7, Application: US/08178482  
 : Patent No. 5629294  
 : GENERAL INFORMATION:  
 : APPLICANT: DIZERCA .. GERE S  
 : APPLICANT: RODGERS .. KATHLEEN E  
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PREVENTING  
 : TITLE OF INVENTION: ADHESION FORMATION  
 : NUMBER OF SEQUENCES: 13  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: ROBBINS, DALGARN, BERLINER & CARSON  
 : STREET: 201 NORTH FIGUEROA STREET, FIFTH FLOOR  
 : CITY: LOS ANGELES  
 : STATE: CALIFORNIA  
 : COUNTRY: USA  
 : ZIP: 90012-2628  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/178,482  
 : FILING DATE: 06-JAN-1994  
 : CLASSIFICATION: 514  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/789,231  
 : FILING DATE: 07-NOV-1991  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: SPITALS .. JOHN P  
 : REGISTRATION NUMBER: 25,215  
 : REFERENCE/DOCKET NUMBER: 1920-314  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (213) 977-100;  
 : TELEFAX: (213) 977-1005  
 : INFORMATION FOR SEQ ID NO: 7:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 6 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : US-08-178-482-7

Query Match 100.0%; Score 35; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 1 GRGDT 6

Db 1 GRGDT 6

## RESULT 3

US-08-234-997-1  
 : Sequence 1, Application US/08234997  
 : Patent No. 5683867  
 : GENERAL INFORMATION:  
 : APPLICANT: SUMEDHA JAYASENA  
 : APPLICANT: GREG BIESECKER  
 : APPLICANT: LARRY GOLD  
 : APPLICANT: DREW SMITH  
 : APPLICANT: GARY KIRSCHENHEUTER  
 : TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY  
 : TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: BLENDED  
 : NUMBER OF SEQUENCES: 5  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Beaton & Swanson, P.C.  
 : STREET: 4582 South Ulster Street Parkway, #403  
 : CITY: Denver

: STATE: Colorado  
 : COUNTRY: USA  
 : ZIP: 80237  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage  
 : COMPUTER: IBM pc compatible  
 : OPERATING SYSTEM: MS-DOS  
 : SOFTWARE: WordPerfect 5.1  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/234,997  
 : FILING DATE:  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 07/714,131  
 : FILING DATE: JUNE 10, 1991  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 07/536,428  
 : FILING DATE: JUNE 11, 1990  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/117,991  
 : FILING DATE: SEPTEMBER 8, 1993  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/123,935  
 : FILING DATE: SEPTEMBER 17, 1993  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/199,507  
 : FILING DATE: FEBRUARY 22, 1994  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Barry J. Swanson  
 : REGISTRATION NUMBER: 33,215  
 : REFERENCE/DOCKET NUMBER:  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (303) 850-9900  
 : TELEFAX: (303) 850-9401  
 : INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 6 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : US-08-234-997-1

Query Match 100.0%; Score 35; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 1 GRGDT 6

Db 1 GRGDT 6

## RESULT 4

US-08-747-137-74  
 : Sequence 74, Application US/08747137  
 : Patent No. 5945033  
 : GENERAL INFORMATION:  
 : APPLICANT: YEN, Richard C.K.  
 : TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR  
 : TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE  
 : NUMBER OF SEQUENCES: 184  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Townsend and Townsend and Crew LLP  
 : STREET: Two Embarcadero Center, 8th Floor  
 : CITY: San Francisco  
 : STATE: CA  
 : COUNTRY: USA  
 : ZIP: 94111  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:

```

1  APPLICATION NUMBER: US 08/747,137
2  FILING DATE: 12-NOV-1996
3  CLASSIFICATION: 424
4  PRIOR APPLICATION DATA:
5  APPLICATION NUMBER: US 08/212,546
6  FILING DATE: 14-MAR-1994
7  PRIOR APPLICATION DATA:
8  APPLICATION NUMBER: US 08/065,831
9  FILING DATE: 01-JUN-1993
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US 07/955,560
12 FILING DATE: 13-OCT-1992
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 07/641,720
15 FILING DATE: 15-JAN-1991
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Apple, Randolph T.
18 REGISTRATION NUMBER: 36,429
19 REFERENCE/DOCKET NUMBER: 016197-0008400S
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: 415-576-0200
22 INFORMATION FOR SEQ ID NO: 34:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 6 amino acids
25 TYPE: amino acid
26 STRANDEDNESS: not relevant
27 TOPOLOGY: not relevant
28 US-08-747-137-74

```

```

Query Match 100.0% Score 35: DB 2: Length 6:
Best Local Similarity 100.0% Pred. No. 2.5e+05:
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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QY 1 GCGDTP 6
DB 1 GCGDTP 5

```

## RESULT 5

```

US-08-747-137-176
1 Sequence 176: Application US/08747137
2 Patent No. 5945033
3 GENERAL INFORMATION:
4 APPLICANT: YEN, Richard C.K.
5 TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
6 THERAPEUTIC AND DIAGNOSTIC USE
7 NUMBER OF SEQUENCES: 184
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Townsend and Townsend and Crew LLP
10 STREET: Two Embarcadero Center, 8th Floor
11 CITY: San Francisco
12 STATE: CA
13 COUNTRY: USA
14 ZIP: 94111
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: 5-copy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent In Release #1.0, Version #1.3G
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/747,137
22 FILING DATE: 12-NOV-1996
23 CLASSIFICATION: 424
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 08/212,546
26 FILING DATE: 14-MAR-1994
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 08/065,831
29 FILING DATE: 01-JUN-1993
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 07/955,560
32 FILING DATE: 13-OCT-1992
33 PRIOR APPLICATION DATA:

```

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1  APPLICATION NUMBER: US 07/641,720
2  FILING DATE: 15-JAN-1991
3  ATTORNEY/AGENT INFORMATION:
4  NAME: Apple, Randolph T.
5  REGISTRATION NUMBER: 36,429
6  REFERENCE/DOCKET NUMBER: 016197-0008400S
7  TELECOMMUNICATION INFORMATION:
8  TELEPHONE: 415-576-0200
9  INFORMATION FOR SEQ ID NO: 176:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 6 amino acids
12 TYPE: amino acid
13 STRANDEDNESS: not relevant
14 TOPOLOGY: not relevant
15 US-08-747-137-176

```

```

Query Match 100.0% Score 35: DB 2: Length 6:
Best Local Similarity 100.0% Pred. No. 2.5e+05:
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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QY 1 GCGDTP 6
DB 1 GCGDTP 6

```

```

RESULT 6
US-08-956-699-1
1 Sequence 1: Application US/089566599
2 Patent No. 6083696
3 GENERAL INFORMATION:
4 APPLICANT: GREG BIESCHKE
5 APPLICANT: SUMEDHA D. JAYASENA
6 APPLICANT: LARRY GOLD
7 APPLICANT: DREW SMITH
8 APPLICANT: GARY P. KIRSCHENHEUTER
9 TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS
10 TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: BLENDED
11 TITLE OF INVENTION: SELEX
12 NUMBER OF SEQUENCES: 5
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: Swanson & Bratschan, L.L.C.
15 STREET: 8400 E. Prentice Avenue, Suite 100
16 CITY: Englewood
17 STATE: Colorado
18 COUNTRY: USA
19 ZIP: 80111
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
22 COMPUTER: IBM pc compatible
23 OPERATING SYSTEM: MS-DOS
24 SOFTWARE: WordPerfect 6.0
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/08/956,699
27 FILING DATE: OCTOBER 23, 1997
28 CLASSIFICATION: 435
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: 08/234,997
31 FILING DATE: APRIL 28, 1994
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: 07/714,131
34 FILING DATE: JUNE 10, 1991
35 PRIOR APPLICATION DATA:
36 APPLICATION NUMBER: 07/536,428
37 FILING DATE: JUNE 11, 1990
38 PRIOR APPLICATION DATA:
39 APPLICATION NUMBER: 08/117,991
40 FILING DATE: SEPTEMBER 8, 1993
41 PRIOR APPLICATION DATA:
42 APPLICATION NUMBER: 08/123,935
43 FILING DATE: SEPTEMBER 17, 1993
44 PRIOR APPLICATION DATA:
45 APPLICATION NUMBER: 08/199,507
46 FILING DATE: FEBRUARY 22, 1994

```

```

1 ATTORNEY/AGENT INFORMATION:
2 NAME: Barry J. Swanson
3 REGISTRATION NUMBER: 33,215
4 REFERENCE/DOCKET NUMBER: NEX15/C
5 TELECOMMUNICATION INFORMATION:
6 TELEPHONE: (303) 793-3333
7 TELEFAX: (303) 793-3433
8 INFORMATION FOR SEQ ID NO: 1:
9 LENGTH: 6 amino acids
10 TYPE: amino acid
11 STRANDEDNESS: single
12 TOPOLOGY: linear
13 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
14 US-08-956-699-1
15
16 Query Match 100.0%; Score 35; DB 3; Length 6;
17 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
18 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
19
20 QY 1 GRGDTF 6
21 DB 1 GRGDTF 6
22
23 RESULT 7
24 US-09-606-477-1
25 : Sequence 1, Application US/03606477
26 : Patent No. 6465189
27 : GENERAL INFORMATION:
28 : APPLICANT: GREG BIESECKER
29 : INVENTOR: LARRY GOLD
30 : DREW SMITH
31 : GARY P. KIRSCHENHEUTER
32 : TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
33 : EXPONENTIAL ENRICHMENT: BLENDSE
34 : SELEX
35 : NUMBER OF SEQUENCES: 5
36 : CORRESPONDENCE ADDRESS:
37 : ADDRESS: Swanson & Bratschus, L.L.C.
38 : STREET: 1745 Shea Center Drive, Suite 310
39 : CITY: Highlands Ranch
40 : STATE: Colorado
41 : COUNTRY: USA
42 : ZIP: 80129
43 : COMPUTER READABLE FORM:
44 : MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
45 : COMPUTER: IBM PC compatible
46 : OPERATING SYSTEM: MS-DOS
47 : SOFTWARE: WordPerfect 8.0
48 : CURRENT APPLICATION DATA:
49 : APPLICATION NUMBER: US/79/606,477
50 : FILING DATE: 29-Jun-2002
51 : CLASSIFICATION: <Unknown>
52 : PRIOR APPLICATION DATA:
53 : APPLICATION NUMBER: 08/956,699
54 : FILING DATE: OCTOBER 23, 1997
55 : APPLICATION NUMBER: 08/234,997
56 : FILING DATE: APRIL 28, 1994
57 : APPLICATION NUMBER: 07/714,133
58 : FILING DATE: JUNE 10, 1991
59 : APPLICATION NUMBER: 07/536,428
60 : FILING DATE: JUNE 11, 1990
61 : APPLICATION NUMBER: 08/117,991
62 : FILING DATE: SEPTEMBER 8, 1993
63 : APPLICATION NUMBER: 08/123,935
64 : FILING DATE: SEPTEMBER 17, 1993
65 : APPLICATION NUMBER: 08/59,507
66 : FILING DATE: FEBRUARY 22, 1994
67 : ATTORNEY/AGENT INFORMATION:
68 : NAME: Barry J. Swanson
69 : REGISTRATION NUMBER: 33,215
70 : REFERENCE/DOCKET NUMBER: NEX15/C-CON
71
72 TELECOMMUNICATION INFORMATION:
73 TELEPHONE: (303) 793-3333
74 TELEFAX: (303) 793-3433
75 INFORMATION FOR SEQ ID NO: 1:
76 LENGTH: 6 amino acids
77 TYPE: amino acid
78 STRANDEDNESS: single
79 TOPOLOGY: linear
80 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
81 US-09-606-477-1
82
83 Query Match 100.0%; Score 35; DB 4; Length 6;
84 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
85 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
86
87 QY 1 GRGDTF 6
88 DB 1 GRGDTF 6
89
90 RESULT 8
91 US-09-485-653-1
92 : Sequence 1, Application US/09485653
93 : Patent No. 655321
94 : GENERAL INFORMATION:
95 : APPLICANT: Daniel, Thomas O.
96 : APPLICANT: Stein, Elke
97 : TITLE OF INVENTION: Methods for Determining Cell Responses
98 : TITLE OF INVENTION: Through EphA Receptors
99 : FILE REFERENCE: 22000.008501
100 : CURRENT APPLICATION NUMBER: US/09/485,653
101 : CURRENT FILING DATE: 2000-02-14
102 : PRIOR APPLICATION NUMBER: PCT/US98/17157
103 : PRIOR FILING DATE: 1998-08-19
104 : PRIOR APPLICATION NUMBER: 60/056,164
105 : PRIOR FILING DATE: 1997-08-19
106 : NUMBER OF SEQ ID NOS: 3
107 : SOFTWARE: FastSeq for Windows Version 4.0
108 : SEQ ID NO 1
109 : LENGTH: 6
110 : TYPE: PRT
111 : ORGANISM: Artificial Sequence
112 : FEATURE:
113 : OTHER INFORMATION: Description of Artificial Sequence: No. 655321c -
114 : OTHER INFORMATION: Synthetic construct
115 : US-09-485-653-1
116
117 Query Match 100.0%; Score 35; DB 4; Length 6;
118 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
119 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
120
121 QY 1 GRGDTF 6
122 DB 1 GRGDTF 6
123
124 RESULT 9
125 US-09-548-697A-2
126 : Sequence 2, Application US/09548697A
127 : Patent No. 6586187
128 : GENERAL INFORMATION:
129 : APPLICANT: American Cyanamid Company
130 : APPLICANT: Gopalsamy, Arimalla
131 : APPLICANT: Yang, Hui Y
132 : TITLE OF INVENTION: Methods for Solid Phase Combinatorial Synthesis of Integrin In
133 : FILE REFERENCE: AHP-98202
134 : CURRENT APPLICATION NUMBER: US/09/548,697A
135 : CURRENT FILING DATE: 2000-04-13
136 : PRIOR APPLICATION NUMBER: 60/240,952
137 : PRIOR FILING DATE: 1999-04-14
138 : NUMBER OF SEQ ID NOS: 9
139 : SOFTWARE: PatentIn version 3.1

```

```

: SEQ ID NO 2
: LENGTH: 6
: TYPE: PRT
: ORGANISM: unknown
: FEATURE:
: OTHER INFORMATION: synthetic
US-09-548-697A-2

Query Match      100.0% Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 GRGDP 6
DB 1 GRGDP 6

RESULT 10
PCT-US93-05640-45
: Sequence 45, Application PCT/US93/05640
: GENERAL INFORMATION:
: APPLICANT: University of Connecticut
: TITLE OF INVENTION: Contraceptive Vaccine
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
: STREET: Two Million Drive
: CITY: Lexington
: STATE: MA
: COUNTRY: USA
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/05640
: FILING DATE: 19930610
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/837,883
: FILING DATE: June 12, 1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Brook, David E.
: REGISTRATION NUMBER: 22,592
: REFERENCE/DOCKET NUMBER: UCT90-01AA
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 861-5240
: TELEFAX: (617) 861-9540
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
PCT-US93-05640-45

Query Match      100.0% Score 35; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 GRGDP 6
DB 1 GRGDP 6

RESULT 11
US-07-720-222-46
: Sequence 46, Application US/07/20222
: Patent No. 5190873
: GENERAL INFORMATION:

```

---

```

: APPLICANT: Lernhardt, Waldemar
: APPLICANT: Bourdon, Mario
: APPLICANT: Youderian, Phil
: TITLE OF INVENTION: HYBRID PROTEINS CONTAINING BINDING SITES
: NUMBER OF SEQUENCES: 58
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Bingham & Pitting
: STREET: 11230 Sorrento Valley Road, Suite 200
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92121
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/20,222
: FILING DATE: 19910621
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Bingham, Douglas A.
: REGISTRATION NUMBER: 32,457
: REFERENCE/DOCKET NUMBER: C180612P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-587-3533
: INFORMATION FOR SEQ ID NO: 46:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids
: TYPE: AMINO ACID
: STRANDEDNESS: single
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
US-07-720-222-46

Query Match      88.6% Score 31; DB 1; Length 5;
Best Local Similarity 83.3%; Pred. No. 2.5e+5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 GRGDP 6
DB 1 GRGDP 6

RESULT 12
US-07-780-790A-6
: Sequence 6, Application US/07/80790A
: Patent No. 5298488
: GENERAL INFORMATION:
: APPLICANT: KOJIMA, Masayoshi
: APPLICANT: KOMAZAWA, Hiroyuki
: TITLE OF INVENTION: CN-CHITIN DERIVATIVES AND USE THEREOF
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sughrue, Mior, Zinn, Macpeak, & Seas
: STREET: 2100 Pennsylvania Avenue
: CITY: Washington
: STATE: District of Columbia
: COUNTRY: USA
: ZIP: 20037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/80,790A
: FILING DATE: 1991023
: CLASSIFICATION: 530

```

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
TELEX: 6491103

## INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-07-780-790A-6

Query Match 88.6%; Score 31; DB 1; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.5e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0;

QY 1 GRGDTP 6  
DB 1 GRGDSP 6

## RESULT 13

US-07-932-200-11

Sequence 11, Application US/07932200

Patent No. 5366862

## GENERAL INFORMATION:

APPLICANT: VENTON, DUANE L.  
APPLICANT: HOPFINGER, ANTON J.

APPLICANT: LE BRETON, GUY

TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING  
NUMBER OF SEQUENCES: 20

## CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 SEVENTH STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20004

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/932,200  
FILING DATE: 21-AUG-1992  
CLASSIFICATION: 4.5

## ATTORNEY/AGENT INFORMATION:

NAME: COOPER, IVER P.

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: VENTON-1H

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

## INFORMATION FOR SEQ ID NO: 11:

## SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-07-932-200-11

Query Match 88.6%; Score 31; DB 1; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.5e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0;

QY 1 GRGDTP 6  
DB 1 GRGDSP 6

## RESULT 14

US-08-234-979-3

Sequence 3, Application US/08234979

Patent No. 5510328

## GENERAL INFORMATION:

APPLICANT: Schreiber, Rondu

APPLICANT: Polarek, James

APPLICANT: Tamura, Richard

APPLICANT: Harper, John

TITLE OF INVENTION: Compositions that inhibit wound

contraction and Methods of using same

NUMBER OF SEQUENCES: 5

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/234,979

FILING DATE: 28-APR-1994

CLASSIFICATION: 514

## ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-1A 9955

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9900

TELEFAX: (619) 535-8949

## INFORMATION FOR SEQ ID NO: 3:

## SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-234-979-3

Query Match 88.6%; Score 31; DB 1; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.5e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0;

QY 1 GRGDTP 6  
DB 1 GRGDSP 6

## RESULT 15

US-08-251-027-13

Sequence 13, Application US/08251027

Patent No. 5519005

## GENERAL INFORMATION:

APPLICANT: Lider, Ofer

APPLICANT: Greenspoon, No. 5519005a

APPLICANT: Hershkoviz, Rami

APPLICANT: Alon, Ronen

TITLE OF INVENTION: A METHOD OF INHIBITION OF CELLULAR AND

MOLECULAR LEVEL BIOLOGICAL INTERACTIONS UTILIZING

NON-PEPTIDIC SURROGATES OF THE ARG-GLY-ASP SEQUENCE

NUMBER OF SEQUENCES: 16

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Kohn & Associates  
STREET: 30500 No. 5519005thwestern Highway, Suite 410  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: U.S.  
ZIP: 48334

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/28/251,627  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Koho, Kenneth I.  
REGISTRATION NUMBER: 30,955  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (813) 539-5950  
TELEFAX: (813) 539-5055  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-08-251-027-13

Query Match 88.6% Score 41 DB 11 Length 6  
Best Local Similarity 83.3% Prod. No. 215e-05  
Matches 5: Conservative 1: Mismatches 0: Gaps 0

QY 1 GRGDP 6  
DB 1 GRGDSP 6

Search completed: September 16, 2003, 16:21:21  
Job time : 17 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2003, 16:17:03 : Search time 38 seconds  
(without alignments)  
25.062 Million cell updates/sec

Title: US-09-780-612A:

Perfect score: 35

Sequence: 1 GRG5P 6

Scoring table:

Gapop 10.0 : Gapext 0.5

Searched: 1:07563 seqs, 158726574 residues

Total number of hits satisfying chosen parameters: 30962

Minimum DB seq length: 6

Maximum DB seq length: 6

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	14	Adhesion formation
2	35	100.0	6	15	P4-30 beta disintegrin
3	35	100.0	6	17	Synthetic protein
4	35	100.0	6	17	RGD peptide, Syn
5	35	100.0	6	20	Neurospiral-activated
6	35	100.0	6	20	Non-crosslinked pr
7	35	100.0	6	20	AA13127
8	35	100.0	6	20	AA13125
9	35	100.0	6	20	AA13125
9	35	100.0	6	20	AA13125

10	35	100.0	6	21	AA190475
11	35	100.0	6	22	AA191972
12	35	100.0	6	23	AA190076
13	31	88.6	6	11	AA1904612
14	31	88.6	6	11	AA1906455
15	31	88.6	6	13	AA1909083
16	31	88.6	6	13	AA1909088
17	31	88.6	6	13	AA1909088
18	31	88.6	6	13	AA1909088
19	31	88.6	6	13	AA1909088
20	31	88.6	6	13	AA1909088
21	31	88.6	6	13	AA1909088
22	31	88.6	6	13	AA1909088
23	31	88.6	6	13	AA1909088
24	31	88.6	6	13	AA1909088
25	31	88.6	6	13	AA1909088
26	31	88.6	6	13	AA1909088
27	31	88.6	6	13	AA1909088
28	31	88.6	6	13	AA1909088
29	31	88.6	6	13	AA1909088
30	31	88.6	6	13	AA1909088
31	31	88.6	6	13	AA1909088
32	31	88.6	6	13	AA1909088
33	31	88.6	6	13	AA1909088
34	31	88.6	6	13	AA1909088
35	31	88.6	6	13	AA1909088
36	31	88.6	6	13	AA1909088
37	31	88.6	6	13	AA1909088
38	31	88.6	6	13	AA1909088
39	31	88.6	6	13	AA1909088
40	31	88.6	6	13	AA1909088
41	31	88.6	6	13	AA1909088
42	31	88.6	6	13	AA1909088
43	31	88.6	6	13	AA1909088
44	31	88.6	6	13	AA1909088
45	31	88.6	6	13	AA1909088

#### ALIGNMENTS

AAR36709  
 AAR36709 standard; peptide; 6 AA.  
 AAR36709:  
 25-MAR-2003 (updated)  
 26-APR-1993 (first entry)  
 Adhesion formation prevention: RGD-contg. peptide.  
 Tissue repair; peritoneum; surgery; post-surgically; inhibition;  
 platelet aggregation; cardiovascular; orthopedic; thoracic;  
 ophthalmic; CNS; use.  
 Synthetic.  
 W09308818-A1.  
 13-MAY-1993.  
 06-NOV-1992; 92WO-US09494.  
 07-NOV-1991; 91US-0789231.  
 (UNSC-) UNIV SOUTHERN CALIFORNIA.  
 Hitzereggs GS. Rodgers KE;  
 WPI: 1993-167381/20.  
 Prevention of adhesion formation, partic. post-surgically - comprises

Cell adhesion pept  
 Fibronectin fragme  
 Integrin modulator  
 Antiviral agent.  
 Fibronectin deri  
 Peptide contg. RGD  
 Peptide contg. RGD  
 Peptide lipid cont  
 Peptide lipid cont  
 Peptide contg. RGD  
 Peptide contg. RGD  
 Gelatin deriv. pep  
 Polyethylene glyco  
 Fragment of tenasc  
 Cell adhesive pept  
 Activation indepen  
 Peptide deriv. con  
 Proten-amide pept  
 PEG-contg. peptide  
 Adhesion formation  
 Adhesion formation  
 Proten-amide deri  
 Fibronogen fragmen  
 GRGSP synthetic p  
 Peptide for isolat  
 Cell adhesion moti  
 RGD peptide deriva  
 Synthetic RGD pept  
 Sequence of peptid  
 Binding site deriv  
 Cancer metastasis  
 Competitor fibron  
 Alpha5/beta1 integ  
 RGD contg. peptide  
 Synthetic, weak, t



PT administering a RGD-contg. peptide for a time sufficient to permit  
 XX tissue repair

Example: Page 18; 22pp; English.

CC The sequence is that of an RGD-contg. peptide which is used in a  
 CC method for prevention of adhesion formation for a time sufficient  
 CC to permit tissue repair. The method is used for minimising or  
 CC preventing adhesion formation, partic. in the peritoneum following  
 CC surgery, but also for e.g. cardiovascular, orthopedic, thoracic,  
 CC ophthalmic, CNS and other uses. In addition, the peptide inhibits  
 CC platelet aggregation and does not induce inflammation or trauma  
 CC at the site of administration.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 14; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GRGDTP 6  
 DB 1 GRGDTP 6

RESULT 2

ID AAR47384  
 AC AAR47384 standard; Protein: 6 AA.

XX AAR47384;

XX 25-MAR-2003 (updated)

DT 22-JUN-1994 (first entry)

DE PH-30 beta disintegrin control peptide.

XX PH-20; PH-30; contraceptive; fertilisation; sperm surface protein;  
 KW vaccine; sperm-egg fusion.

XX Rubella virus.

XX WO9325233-A1.

XX 23-DEC-1993.

XX 10-JUN-1993; 93WO-US05540.

XX 12-JUN-1992; 92US-0897383.

XX (UYCO-) UNIV CONNECTICUT.

XX Myles DG, Primakoff P;

XX WPI; 1994-007200/01.

XX Contraceptive vaccine for reducing sperm-egg fusion - comprises  
 PT peptide from sperm surface protein which stimulates antibody  
 PT prodn.

XX Example 7; Page 27; 79pp; English.

XX Example 7 describes the use of PH-30 beta disintegrin peptides  
 CC as inhibitors of sperm fusion to egg plasma membrane.

CC Modified peptides AAR47382-83 and control peptides (AAR47384-85)  
 CC were tested. From observations it was concluded that the  
 CC PH-30 beta disintegrin domain represents an epitope which  
 CC is critical in sperm-egg fusion.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 15; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GRGDTP 6  
 DB 1 GRGDTP 6

RESULT 3

ID AAW07430 standard; peptide: 6 AA.

XX AAW07430;

XX 25-MAR-2003 (updated)

DT 21-JAN-1997 (first entry)

XX Synthetic, preferred tumour invasion-inhibitory peptide.

XX Tumour invasion; extracellular matrix; ECM; metastasis; RGD sequence;  
 KW cancer; inhibition; control.

XX Synthetic.

XX US5547936-A.

XX 20-AUG-1996.

XX 17-DEC-1993; 93US-0169743.

XX 17-DEC-1993; 93US-0169743.

XX 22-NOV-1983; 83US-0554821.

XX 17-JUN-1985; 85US-0744981.

XX 10-MAR-1988; 88US-0166530.

XX 09-SEP-1988; 88US-0242713.

XX 25-FEB-1991; 91US-0660526.

XX 10-APR-1991; 91US-0883585.

XX 08-OCT-1991; 91US-0773106.

XX 19-JUN-1992; 92US-0902742.

XX (JOL-) LA JOLLA CANCER RES FOUND.

XX Gehlsen KR, Pierschbacher MD, Ruoslahti E;

XX WPI; 1996-392651/39.

XX Inhibiting tumour cell invasion through an extracellular matrix -  
 PT using peptide contg. the RGD sequence, partic. for preventing tumour  
 PT metastasis

XX Claim 2; Column 7-8; 8pp; English.

XX AAW07430 is a preferred peptide identified in an assay for testing  
 CC peptides for tumour-invasion inhibitory activity. The peptides  
 CC (contg. the RGD sequence) shows significant inhibition of tumour  
 CC invasion of the ECM. Other peptides tested (see AAW07431-W06433) did  
 CC show inhibitory activity but to a lesser extent than peptide AAW07430  
 CC The peptides identified can be used to treat cancer and to prevent  
 CC metastasis, in partic. invasion of the extracellular matrix (ECM).  
 CC The peptides are soluble.  
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 17; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GRGDTP 6  
 DB 1 GRGDTP 6



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PN US5945033-A.
XX
PD 31-AUG-1999.
XX
PF 12-NOV-1996; 96US-0747137.
XX
PR 14-MAR-1994; 94US-0212546.
PR 15-JAN-1991; 91US-0641720.
PR 13-OCT-1992; 92US-0953560.
PR 01-JUN-1993; 93US-0065831.
PR 12-NOV-1996; 96US-0747137.
XX
PA (HEMO-) HEMOSPHERE INC.
XX
PI Yen RCK;
XX
DR WPI: 1999-508153/42.
XX
PT Non-crosslinked protein particles for therapeutic and diagnostic use
XX
PS Example 22; Column 81-82; 65pp; English.
XX
CC This invention describes a novel aqueous suspension of monodisperse
CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which
CC is stable against dissolving upon dilution with an alcohol-free aqueous
CC medium. The method involves (a) forming an aqueous solution containing
CC albumin and hemoglobin and (b) treating the aqueous solution with an
CC alcohol to cause the solution to become turbid. The particles are useful
CC as agents for in vivo administration, either of their own administration
CC or as a vehicle for other therapeutic or diagnostic agents. The method
CC permits the formation of albumin and hemoglobin particles in the
CC nanometer and micrometer size range, in a form closer to their natural
CC form than the forms of the prior art. The particles therefore constitute
CC a more closely controlled agent for in vivo administration, with greater
CC ease of clearance from the body after their period of usefulness.
CC AAY30952-Y31135 represent peptides used in the method of the invention.
XX
SQ Sequence 6 AA:
Query Match 100.0%; Score 35; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GRGTRP 6
DB 1 GRGTRP 6
RESULT 7
AAY31025
ID AAY31025 standard; peptide: 6 AA.
XX
AC AAY31025;
XX
DT 21-OCT-1999 (first entry)
XX
DE Non-crosslinked protein particle peptide 74.
XX
KW Non-crosslinked protein particles; diagnostic; therapy; monodisperse;
KW albumin; haemoglobin; nanometer; micrometer; clearance.
XX
OS Synthetic.
XX
PN US5945033-A.
XX
PD 31-AUG-1999.
XX
PF 12-NOV-1996; 96US-0747137.
XX
PR 14-MAR-1994; 94US-0212546.
PR 15-JAN-1991; 91US-0641720.
PR 13-OCT-1992; 92US-0953560.
PR 01-JUN-1993; 93US-0065831.
XX

```

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```

PA 12-NOV 1996; 96US-0747137.
XX
PA (HEMO-) HEMOSPHERE INC.
XX
PI Yen RCK;
XX
DR WPI: 1999-508153/42.
XX
PT Non-crosslinked protein particles for therapeutic and diagnostic use
XX
PS Example 22; Column 81-82; 65pp; English.
XX
CC This invention describes a novel aqueous suspension of monodisperse
CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which
CC is stable against dissolving upon dilution with an alcohol-free aqueous
CC medium. The method involves (a) forming an aqueous solution containing
CC albumin and hemoglobin and (b) treating the aqueous solution with an
CC alcohol to cause the solution to become turbid. The particles are useful
CC as agents for in vivo administration, either of their own administration
CC or as a vehicle for other therapeutic or diagnostic agents. The method
CC permits the formation of albumin and hemoglobin particles in the
CC nanometer and micrometer size range, in a form closer to their natural
CC form than the forms of the prior art. The particles therefore constitute
CC a more closely controlled agent for in vivo administration, with greater
CC ease of clearance from the body after their period of usefulness.
CC AAY30952-Y31135 represent peptides used in the method of the invention.
XX
SQ Sequence 6 AA:
Query Match 100.0%; Score 35; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GRGTRP 6
DB 1 GRGTRP 6
RESULT 8
AAY84459
ID AAY84459 standard; Peptide: 6 AA.
XX
AC AAY84459;
XX
DT 25-MAR-1999 (first entry)
XX
DE RGD peptide that stimulates cell invasion by S. pyogenes 90 226.
XX
KW Streptococcus pyogenes 90-226; pathogen; inhibition;
KW cell adhesion; cell invasion; treatment; bacterial; infection;
KW fungal infection.
XX
OS Synthetic.
XX
PN WO9856438-A2.
XX
DT 17-DEC-1996.
XX
PR 10-JUN-1998; 98WO-US12019.
XX
PR 10-JUN-1997; 97US-0049124.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Cleary PP, Cue DR;
XX
DR WPI: 1999-080856/07.
XX
PT Method for treating mammal infected by pathogenic microorganism -
PT comprises administering to mammal composition comprising inhibitory
PT compound which inhibits adherence to or invasion of a cell by
PT microorganism
XX

```

PS Example 2; Page 43; 58pp; English.

XX The present sequence represents a RGD peptide that is able to  
CC stimulate cell invasion by Streptococcus pyogenes 93-225. The  
CC peptides were used in the course of the invention. The  
CC specification describes the treatment of a mammal infected  
CC by a pathogenic microorganism which comprises administering an  
CC inhibitory compound to inhibit adherence to or invasion of cells  
CC by the pathogen. The method is used in the treatment of bacterial  
CC or fungal infection.

XX Sequence 6 AA;

Query Match 100.0%; Score 35; E6 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTTP 6  
Db 1 GRGDTTP 6

RESULT 9  
AA528163  
ID AAB28163 standard; peptide: 6 AA.

XX AC AA528163;  
XX DT 09-FEB-2000 (first entry)

XX Peptide #3 used to assay vitronectin receptor binding inhibition.

XX Antiviral; antiinflammatory; cytostatic; vasotropic; antitumour;  
KW antiarthritic; ophthalmological; osteopathic;  
KW amido-carboxylic acid derivative; cancer; angiogenesis;  
KW neovascularisation; macular degeneration; glaucoma; blindness;  
KW rheumatoid arthritis; restenosis; viral infection; bone resorption;  
KW osteoporosis; osteopenia; periodontal disease; hyperparathyroidism;  
KW Paget's disease; integrin vitronectin receptor; alpha\_vbeta\_3; melanoma.

XX Unidentified.

XX WO2000061545-A1.

XX 19-OCT-2000.

XX 13-APR-2000; 2000WO-US10027.

XX 14-APR-1999; 99US-0291470.

XX (AMHP ) AMERICAN HOME PROD CORP.

XX Gopalasamy A, Yang HY;

XX WPI; 2000-687029/67.

XX New amido-carboxylic acid derivatives are integrin inhibitors used for  
PT treating e.g. cancer, restenosis, osteoporosis, viral infection and  
PT bone disease.

XX Disclosure; Page 17; 67pp; English.

XX The present invention relates to amido-carboxylic acid derivatives. The  
CC amido-carboxylic acid derivatives may be used for treating cancer,  
CC angiogenesis, neovascularisation, macular degeneration, glaucoma,  
CC blindness, rheumatoid arthritis, restenosis, smooth cell proliferation  
CC and migration, vascular endothelial cell proliferation and migration,  
CC viral infection (characterised by bone resorption of mineralised  
CC tissues), osteoporosis, hypercalcaemia of malignancy, osteopenia due to  
CC bone metastasis, periodontal disease, hyperparathyroidism, periarticular  
CC erosions in rheumatoid arthritis, Paget's disease, immobilisation-induced  
CC osteopenia or glucocorticoid treatment, or diseases characterised by some  
CC resorption of mineralised tissues. The present sequence is a peptide.

CC which was used as a reference compound in an assay for the ability of the  
CC amido-carboxylic acid derivatives of the present invention to inhibit  
CC integrin vitronectin receptor (alpha\_vbeta\_3) binding. Integrin  
CC alpha\_vbeta\_3 has been shown to mediate the invasion of cancerous  
CC melanoma cells into healthy tissue and to protect these cells against  
CC apoptosis. In addition, vitronectin receptor antagonists have been shown  
CC to inhibit the growth of various solid tumours of human origin.

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTTP 6  
Db 1 GRGDTTP 6

RESULT 10  
AA586475  
ID AAY86475 standard; peptide: 6 AA.

XX AC AAY86475;  
XX XT 06-JUN-2000 (first entry)

XX Cell adhesion peptide #10.

XX Bone regenerative; osteopathic; osseous tissue; reconstitution;  
KW scaffold matrix; bone formation promoter; bone resorption inhibitor;  
KW cell adhesion; osteoblast; osteoclast; bone defect; fracture.

XX Synthetic.

XX WO200004941-A1.

XX 03-FEB-2000.

XX 22-JUL-1999; 99WO-US16800.

XX 24-JUL-1996; 98US-012348.

XX (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.

XX Sudny JA;

XX WPI; 2000-195084/17.

XX System for reconstructing osseous tissue, useful e.g. for treating  
PT fractures, comprises scaffold containing promoter of bone formation and  
PT inhibitor of bone resorption.

XX Claim 14; Page 31; 44pp; English.

XX The invention relates to a novel system for reconstruction of osseous  
CC tissue comprising a scaffold carrying a compound (I) that promotes  
CC bone formation and a component that decreases bone resorption (II).  
CC (I) induces migration and adhesion of osteoblasts and osteoclasts and  
CC (II) inhibits proteolysis (specifically by plasmin) of extracellular  
CC matrix. (I) is preferably selected from: selectin or selectin binding  
CC fragments, proteins and peptides that facilitate cell adhesion,  
CC plasminogen activator inhibitors, protease inhibitors and  
CC metalloprotease inhibitors. The peptides AAY80466-Y80492 are claimed  
CC examples of cell adhesion peptides used in the system of the invention.  
CC The system is used to replace, remodel or correct bone defects, e.g.  
CC fractures, fissures or bone mass loss. Incorporation of (I) into the  
CC scaffold results in rapid seeding by osteoblasts and the development of  
CC an organic matrix, i.e. the preformed scaffold replaces the  
CC rate-determining step of extracellular matrix formation. The scaffold can  
CC be designed to have a predetermined resorption/degradation rate, and may  
CC include regulatory compounds for specific cell types.

SQ Sequence 6 AA;  
 Query Match 100.0%; Score 35; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTF 6  
 DB 1 GRGDTF 6

RESULT 11  
 AAB91972  
 ID AAB91972 standard; peptide: 6 AA.  
 XX  
 AC AAB91972;  
 XX  
 DT 22-JUN-2001 (first entry)  
 XX  
 DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1149.  
 XX  
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimide; maleimide group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200069900-A2.  
 XX  
 XX 23-NOV-2000.  
 XX  
 PF 17-MAY-2000; 2000WO-US13576.  
 XX  
 PR 17-MAY-1999; 99US-0134406.  
 PR 10-SEP-1999; 99US-0153406.  
 PR 15-OCT-1999; 99US-0159783.  
 XX  
 PA (CONJ-) CONJUCHEM INC.  
 XX  
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
 PI WPI: 2001-1-2059/12.  
 XX  
 DR Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity  
 PT  
 XX  
 XX Disclosure; Page 571; 733pp; English.  
 PS  
 XX The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimide and maleimide groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as binding to large molecules increases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 35; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTF 6  
 DB 1 GRGDTF 6

RESULT 12  
 ABB80076  
 ID ABB80076 standard; peptide: 6 AA.  
 XX  
 AC ABB80076;  
 XX  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE Integrin modulator peptide #3.  
 XX  
 KW Neurodegenerative disease; amyloid; neuroprotective; anti Alzheimer's;  
 KW Alzheimer's disease; integrin; therapeutic agent.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200226107-A2.  
 XX  
 PF 04-APR-2002.  
 XX  
 PF 25-SEP-2001; 2001WO-US29788.  
 XX  
 PR 25-SEP-2000; 2000US-235374P.  
 XX  
 PA (KESC ) UNIV CALIFORNIA.  
 XX  
 XX Lynch G, Xiaoning B, Gall CW;  
 PI WPI: 2002-415420/44.  
 XX  
 DR Experimental models for studying neurodegenerative diseases associated with amyloid accumulation, useful for studying e.g. Alzheimer's disease and for identifying potential therapeutic agents -  
 PT  
 PT  
 XX Claim 15; Page 63; 80pp; English.  
 PS  
 XX The invention relates to experimental models for studying neurodegenerative diseases associated with amyloid accumulation. The activity of peptides of the invention may be described as neuroprotective and anti-Alzheimer's. They act by inhibiting amyloid accumulation. The experimental model may be used to study neurodegenerative diseases associated with amyloid accumulations, e.g. Alzheimer's disease and to identify potential therapeutic agents for treating those diseases. The current sequence represents an integrin modulator peptide of the invention.  
 CC  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 35; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTF 6  
 DB 1 GRGDTF 6

RESULT 13  
 AAR64612  
 ID AAR64612 standard; protein; 6 AA.  
 XX  
 AC AAR64612;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 05-SEP-1990 (first entry)  
 XX  
 DE Antiviral agent.  
 XX

KW Antiviral; M2; poliovirus; folio; hepatitis.  
 OS Synthetic.  
 XX JP02078631-A.  
 PN  
 XX 19-MAR-1990.  
 PD  
 XX 14-SEP-1988; 8BJP-0228943.  
 PF  
 XX 14-SEP-1988; 8BJP-0228843.  
 PR  
 XX (NIHA ) NIPPON MENINS CO.  
 PA  
 XX WPI; 1990-129060/17.  
 DR  
 XX Antiviral agent contg. tripeptide (unit) -  
 PT of basic aminoacid, then alanine, glycine or sarcosine, and  
 PT acidic aminoacid, effective against virus with protein-terminated RNA  
 PT or RNA.  
 XX Disclosure; Page 2; 4pp; Japanese.  
 PS  
 XX Peptide is effective against inhibiting propagation of DNA or RNA  
 CC bonded, protein containing viruses ex. Poliovirus, Hepatitis virus.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 6 AA;  
 Query Match 88.6%; Score 31; DR 11; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.3e-05;  
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 GRGDTP 6  
 DB 1 GRGDSP 6  
 II:II  
 RESULT 14  
 AAR06455  
 ID AAR06455 standard; peptide; 6 AA.  
 XX AAR06455;  
 AC  
 XX 25-MAR-2004 (updated)  
 DT 04-JAN-1991 (first entry)  
 DI  
 XX Fibronectin derived RGD-contg. peptide.  
 DE  
 XX Tenascin; receptor; tumour.  
 KW  
 XX Synthetic.  
 OS  
 XX WO9008781-A.  
 PN  
 XX 09-AUG-1990.  
 PD  
 XX 23-JAN-1990; 90WO-US00408.  
 PE  
 XX 24-JAN-1989; 89US-0302755.  
 PR  
 XX (LJOL-) LA JOLLA CANCER RES FOUND.  
 PA  
 XX Ruoslahti Et., Bourdon MA;  
 PI  
 XX WPI; 1990-260895/34.  
 DR  
 XX Tenascin-induced cell attachment - interacts with tenascin in  
 PT arginine-glycine-asparagine dependent manner.  
 XX  
 PS Example II; Page 9; 22pp; English.  
 XX  
 CC The peptide was used in cell attachment assays to show inhibition.

CC of attachment to tenascin by Arg-Gly Asp contg. peptides. It  
 CC completely inhibited attachment at a concn. of 300-900 µg/ml. 30- and  
 CC 50-fold lower than needed for comparable inhibition of cell  
 CC attachment to vitronectin and fibronectin resp.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 6 AA;  
 Query Match 88.6%; Score 31; DR 11; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.3e-05;  
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 GRGDTP 6  
 DB 1 GRGDSP 6  
 II:II  
 RESULT 15  
 AAR29063  
 ID AAR29063 standard; peptide; 6 AA.  
 XX AAR29063;  
 AC  
 XX 20-MAY-1998 (first entry)  
 DT  
 XX Peptide contg. RGD motif as a side chain to a water sol. polymer.  
 DE  
 XX Adhesive peptide; cell adhesion; inhibitor; platelet aggregation.  
 KW  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 PH Modified\_site 1  
 PT Modified\_site 6 /note= "alkylated/arylated"  
 PE Modified\_site 6 /note= "alkylated/arylated"  
 PF JP04221396-A.  
 PN 11-AUG-1992.  
 DI  
 XX 20-DEC-1990; 90JP-0404347.  
 PF  
 XX 20-DEC-1990; 90JP-0404347.  
 PE  
 XX (FUJF ) FUJI PHOTO FILM CO LTD.  
 PA  
 XX WPI; 1992-313680/38.  
 CR  
 XX Water-soluble vinyl polymer deriv. for animal cell adhesion  
 PI inhibitor or platelet aggregation inhibitor  
 PI  
 XX Example; Page 12; 14pp; Japanese.  
 PS  
 XX The peptide sequence contains the Arg-Gly-Asp motif of cell  
 CC adhering proteins. It comprises the essential unit of a  
 CC water-sol. vinyl polymer with a pref. mol. wt. of 3000-100,000 D.  
 CC The polymer shows various biological activities, e.g. immunological  
 CC coordination, wound healing action and platelet aggregation inhibiting  
 CC action etc. See also AAR29062-8.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 88.6%; Score 31; DR 13; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.3e-05;  
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 GRGDTP 6  
 DB 1 GRGDSP 6  
 II:II

Search completed: September 16, 2003. 18:19:41



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 16, 2003, 15:19:48 : Search time 25 Seconds  
(without alignments)  
35.734 Million cell updates/sec

Title: US-09-780-612A 1  
Perfect score: 35  
Sequence: 1 GRGDTP 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 3.5

Searched: 556269 seqs, 14889369 residues

Total number of hits satisfying chosen parameters: 15287

Minimum DB seq length: 3  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 10%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/pubpa/PCT\_NEW\_PUB.pep:  
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12: /cgn2\_6/ptodata/2/pubpa/US09\_NEW\_PUB.pep:  
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14: /cgn2\_6/ptodata/2/pubpa/US10B\_PUBCOMB.pep:  
15: /cgn2\_6/ptodata/2/pubpa/US10C\_PUBCOMB.pep:  
16: /cgn2\_6/ptodata/2/pubpa/US10\_NEW\_PUB.pep:  
17: /cgn2\_6/ptodata/2/pubpa/US60\_NEW\_PUB.pep:  
18: /cgn2\_6/ptodata/2/pubpa/US60\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	12	US-10-420-029-1
2	35	100.0	6	14	US-10-007-270-35
3	35	100.0	6	15	US-10-263-455-1
4	31	88.6	6	9	US-09-847-969A-26
5	31	88.6	6	9	US-09-847-969A-46
6	31	88.6	6	9	US-09-848-260-15
7	31	88.6	6	9	US-09-961-834-1
8	31	88.6	6	10	US-09-364-597A-21
9	31	88.6	6	10	US-09-177-843-1
10	31	88.6	6	10	US-09-841-321A-28
11	31	88.6	6	10	US-09-841-321A-46
12	31	88.6	6	10	US-09-871-974-3
13	31	88.6	6	10	US-09-972-772-31
14	31	88.6	6	12	US-10-262-435-5
15	31	88.6	6	12	US-10-325-021-9

16	31	88.6	6	14	US-10-031-945-41
17	31	88.6	6	14	US-10-007-270-32
18	31	88.6	6	14	US-10-007-270-35
19	31	88.6	6	14	US-10-114-176-2
20	31	88.6	6	15	US-10-046-801-5
21	31	88.6	6	15	US-10-237-850-83
22	31	88.6	6	15	US-10-136-935-31
23	29	82.9	6	10	US-09-963-206B-10
24	29	82.9	6	10	US-09-916-940-3
25	29	82.9	6	10	US-09-792-630-54
26	29	82.9	6	10	US-09-965-976A-10
27	29	82.9	6	12	US-10-086-550-5
28	29	82.9	6	14	US-10-080-376-54
29	29	82.9	6	14	US-10-061-395-2
30	29	82.9	6	15	US-10-053-355A-7
31	27	77.1	6	9	US-09-765-085-17
32	27	77.1	6	10	US-09-364-597A-23
33	27	77.1	6	10	US-09-177-843-2
34	27	77.1	6	12	US-10-375-942-17
35	27	77.1	6	12	US-10-420-029-2
36	27	77.1	6	15	US-10-237-850-84
37	27	77.1	6	15	US-10-264-374-17
38	25	71.4	5	11	US-09-911-569-31
39	25	71.4	5	12	US-10-200-879-31
40	25	71.4	5	12	US-10-325-021-23
41	25	71.4	6	9	US-09-892-071-5
42	25	71.4	6	11	US-09-911-569-14
43	25	71.4	6	12	US-10-230-879-14
44	25	71.4	6	14	US-10-007-270-34
45	24	68.6	5	9	US-09-096-749A-72

## ALIGNMENTS

RESULT 1  
US-10-420-029-1  
: Sequence 1, Application US10420029  
: Publication No. US20030157712A1  
: GENERAL INFORMATION:  
: APPLICANT: Daniel, Thomas O.  
: APPLICANT: Stein, Elke  
: TITLE OF INVENTION: Methods for Determining Cell Responses  
: TITLE OF INVENTION: Through FpRB Receptors  
: FILE REFERENCE: 22000.508502  
: CURRENT APPLICATION NUMBER: US10/420,029  
: CURRENT FILING DATE: 2003-04-17  
: PRIOR APPLICATION NUMBER: 09/485,653  
: PRIOR FILING DATE: 2000-02-14  
: PRIOR APPLICATION NUMBER: PCT/US98/17157  
: PRIOR FILING DATE: 1998-08-19  
: PRIOR APPLICATION NUMBER: 60/056,164  
: PRIOR FILING DATE: 1997-08-19  
: NUMBER OF SEQ ID NOS: 3  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 1  
: LENGTH: 6  
: TYPE: PRT  
: ORGANISM: Artificial Sequence  
: FEATURE:  
: OTHER INFORMATION: Description of Artificial Sequence; No. US20030157712A1e -  
: OTHER INFORMATION: synthetic construct  
US-10-420-029-1

Query Match 100.0% Score 15; DB 12; Length 6;

Best Local Similarity 100.0% Pred. No. 5e+05; 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

CY 1 GRGDTP 6

DB 1 GRGDTP 6



RESULT 2  
 US-10-007-270-33  
 ? Sequence 33, Application US/10007270  
 ? Publication No. US20020160954A;  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Hagaman, Gregory S.  
 ? APPLICANT: Kuhn, Markus H.  
 ? APPLICANT: University of Iowa Research Foundation  
 ? TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
 ? FILE REFERENCE: 020618-00312005  
 ? CURRENT APPLICATION NUMBER: US/10/007,270  
 ? CURRENT FILING DATE: 2001-11-30  
 ? PRIOR APPLICATION NUMBER: US 03/430,195  
 ? PRIOR FILING DATE: 1999-10-29  
 ? PRIOR APPLICATION NUMBER: US 09/183,472  
 ? PRIOR FILING DATE: 1998-10-29  
 ? NUMBER OF SEQ ID NOS: 37  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO 33  
 ? LENGTH: 6  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence:  
 ? OTHER INFORMATION: RGD-containing peptide  
 ? US-10-007-270-33

Query Match 100.0% Score 35; DB 14; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 50-05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTG 6  
 DB 1 GRGDTG 6

RESULT 3  
 US-10-263-456-1  
 ? Sequence 1, Application US/10263456  
 ? Publication No. US20030077646A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: GREG BIESECKER  
 ? SCMEDHA D. JAYASENA  
 ? LARRY GOLD  
 ? DREW SMITH  
 ? GARY P. KIRSCHENHEUER  
 ? TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY  
 ? EXPONENTIAL ENRICHMENT: BLENDED  
 ? SELEX  
 ? NUMBER OF SEQUENCES: 5  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Swanson & Bratscher, L.L.C.  
 ? STREET: 2745 Shea Center Drive, Suite 310  
 ? CITY: Highlands Ranch  
 ? STATE: Colorado  
 ? COUNTRY: USA  
 ? ZIP: 80129  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: MS-DOS  
 ? SOFTWARE: WordPerfect 8.0  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/10/263,456  
 ? FILING DATE: 02-Oct-2002  
 ? CLASSIFICATION: <Unknown>  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: US/09/605,477  
 ? FILING DATE: 29-Jun-2000  
 ? APPLICATION NUMBER: 08/956,699  
 ? FILING DATE: OCTOBER 23, 1997  
 ? APPLICATION NUMBER: 08/234,997  
 ? FILING DATE: APRIL 26, 1994

APPLICATION NUMBER: 07/714,131  
 FILING DATE: JUNE 10, 1991  
 APPLICATION NUMBER: 07/536,428  
 FILING DATE: JUNE 11, 1990  
 APPLICATION NUMBER: 08/177,991  
 FILING DATE: SEPTEMBER 8, 1993  
 APPLICATION NUMBER: 08/123,935  
 FILING DATE: SEPTEMBER 17, 1993  
 APPLICATION NUMBER: 08/199,507  
 FILING DATE: FEBRUARY 22, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barry J. Swanson  
 REGISTRATION NUMBER: 33,215  
 REFERENCE/DOCKET NUMBER: NEX15/L-CON  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 793-3339  
 TELEFAX: (303) 793-3453  
 ? INFORMATION FOR SEQ ID NO: 1:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 6 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US 10-263-456-1

Query Match 100.0% Score 35; DB 15; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 50-05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTG 6  
 DB 1 GRGDTG 6

RESULT 4  
 US-09-837-969A-28  
 ? Sequence 28, Application US/09837969A  
 ? Patent No. US20020038150A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Urry, Dan  
 ? TITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration  
 ? FILE REFERENCE: BERL-020/0305  
 ? CURRENT APPLICATION NUMBER: US/09/837,969A  
 ? CURRENT FILING DATE: 2001-06-19  
 ? PRIOR APPLICATION NUMBER: US 09/258,723  
 ? PRIOR FILING DATE: 1999-02-26  
 ? PRIOR APPLICATION NUMBER: US 60/087155  
 ? PRIOR FILING DATE: 1998-05-29  
 ? PRIOR APPLICATION NUMBER: US 60/076297  
 ? PRIOR FILING DATE: 1998-02-27  
 ? NUMBER OF SEQ ID NOS: 65  
 ? SOFTWARE: PatentIn version 3.0  
 ? SEQ ID NO 28  
 ? LENGTH: 6  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? NAME/KEY: PEPTIDE  
 ? LOCATION: (1)..(6)  
 ? OTHER INFORMATION: Synthetic  
 ? US-09-837-969A-28

Query Match 88.6% Score 31; DB 9; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 50-05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTG 6  
 DB 1 GRGDTG 6

RESULT 5

```

US-09-837-969A-46
; Sequence 46, Application US/09837969A
; Patent No. US20020038103A1
; GENERAL INFORMATION:
; APPLICANT: Urry, Dan
; TITLE OF INVENTION: Infectable Implants For Tissue Augmentation and Res-Gratification
; FILE REFERENCE: BERL-020/0305
; CURRENT APPLICATION NUMBER: US/09/837,969A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/258,723
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 60/087155
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: US 60/076297
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(6)
; OTHER INFORMATION: Synthetic
US-09-837-969A-46

Query Match      88.6%; Score 31; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 5e-05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDIP 6
   |||||
Db 1 GRGDSP 6

RESULT 6
US-09-888-260-15
; Sequence 15, Application US/09888260
; Patent No. US20020068304A1
; GENERAL INFORMATION:
; APPLICANT: Bioclastics Research, Ltd.
; APPLICANT: Urry, Dan
; TITLE OF INVENTION: Hioelastomer Nanomachines and Biosensors
; FILE REFERENCE: BERL-030/2105
; CURRENT APPLICATION NUMBER: US/09/888,260
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/213,364
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(6)
; OTHER INFORMATION: Synthetic
US-09-888-260-15

Query Match      88.6%; Score 31; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 5e-05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDIP 6
   |||||
Db 1 GRGDSP 6

US-09-837-969A-46
; Patent No. US20020081726A1
; GENERAL INFORMATION:
; APPLICANT: Russell et al.
; TITLE OF INVENTION: MICROFABRICATION OF MEMBRANES FOR THE GROWTH OF CELLS
; FILE REFERENCE: 27611/37761
; CURRENT APPLICATION NUMBER: US/09/961,814
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/235,094
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Fibronectin ligand receptor
US-09-961-834-1

Query Match      88.6%; Score 31; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 5e-05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDIP 6
   |||||
Db 1 GRGDSP 6

REFSLI 8
US-09-364-597A-21
; Sequence 21, Application US/09364597A
; Patent No. US20020103130A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: No. US20020103130A1: Intracellular Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,597A
; FILING DATE: 30-JUL-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/158,001
; FILING DATE: 24-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,861
; FILING DATE: 04-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 3419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 535-9001
; TELEFAX: (858) 535-8949
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-364-597A-21

Query Match      88.6%; Score 31; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 5e-05;

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Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6  
1111  
DB 1 GRGDP 6

## RESULT 3

US-09-177-843-1  
Sequence 1, Application US/0917784;  
Patent No. US20020114804A1  
GENERAL INFORMATION:  
APPLICANT: THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE  
CITY OF NEW YORK  
TITLE OF INVENTION: A METHOD OF PREVENTING AND TREATING  
TITLE OF INVENTION: BACTERIAL INFECTION OF SUTURES AND  
TITLE OF INVENTION: PROSTHETIC DEVICES, AND PROMOTING  
TITLE OF INVENTION: INGRESS OF LEUKOCYTES INTO TUMOR  
TITLE OF INVENTION: FOCI  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1165 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/177,843  
FILING DATE: April 22, 1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 48940-A-PCT/JPW/JKM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

US-09-177-843-1

Query Match 88.6%; Score 31; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. Seqs: 1;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6  
1111  
DB 1 GRGDP 6

## RESULT 10

US-09-841-321A-28  
Sequence 28, Application US/09841321A  
Patent No. US20020116069A1  
GENERAL INFORMATION:  
APPLICANT: Urry, Dan  
TITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration  
FILE REFERENCE: BERL-020/0405  
CURRENT APPLICATION NUMBER: US/09/841,321A  
CURRENT FILING DATE: 2001-04-30

PRIOR APPLICATION NUMBER: US 09/258,723  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: US 60/087155  
PRIOR FILING DATE: 1998-05-23  
PRIOR APPLICATION NUMBER: US 60/076297  
PRIOR FILING DATE: 1998-02-27  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 28  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)...(6)  
OTHER INFORMATION: Synthetic  
US-09-841-321A-28

US-09-841-321A-28

Query Match 88.6%; Score 31; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. Seqs: 1;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6  
1111  
DB 1 GRGDP 6

## RESULT 11

US-09-841-321A-46  
Sequence 46, Application US/09841321A  
Patent No. US20020116069A1  
GENERAL INFORMATION:  
APPLICANT: Urry, Dan  
TITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration  
FILE REFERENCE: BERL-020/0405  
CURRENT APPLICATION NUMBER: US/09/841,321A  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: US 09/258,723  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: US 60/087155  
PRIOR FILING DATE: 1998-05-23  
PRIOR APPLICATION NUMBER: US 60/076297  
PRIOR FILING DATE: 1998-02-27  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 46  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)...(6)  
OTHER INFORMATION: Synthetic  
US-09-841-321A-46

US-09-841-321A-46

Query Match 88.6%; Score 31; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. Seqs: 1;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6  
1111  
DB 1 GRGDP 6

## RESULT 12

US-09-871-974-3  
Sequence 3, Application US/09871974  
Patent No. US20020147136A1  
GENERAL INFORMATION:  
APPLICANT: VON WRONSKI, MATHEW A.  
APPLICANT: MARINELLI, EDMUND R.  
APPLICANT: NUNN, ADRIAN D.  
APPLICANT: PILLAI, RADHAKRISHNA

```

; APPLICANT: RAMALINGAM, KONDAREDDIPATI
; APPLICANT: TREWBLE, MICHAEL F.
; APPLICANT: LINDER, KAREN
; APPLICANT: NARAYANAN, PALANIAPPA
; APPLICANT: RAJU, NATARAJAN
; TITLE OF INVENTION: COMPOUNDS FOR TARGETING ENDOTHELIAL CELLS, COMPOSITIONS
; FILE REFERENCE: 2238-7
; CURRENT APPLICATION NUMBER: US/09/871,974
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 09/585,364
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-871-974-3

Query Match      88.6%   Score 31: DB 10: Length 6:
Best Local Similarity 83.3%   Pred. No. 5e+05:
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 GRGDTP 6
Db 1 GRGDSP 6

RESULT 13
US-09-772-772-31
; Sequence 31: Application US/09/772772
; Publication No. US20020193298A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Gary L.
; APPLICANT: Seif, Christopher
; APPLICANT: Lee, Lily
; APPLICANT: Cook, Charles M.
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
; FILE REFERENCE: PPT-106CP
; CURRENT APPLICATION NUMBER: US/09/772-772
; CURRENT FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 09/704,251
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 31
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motifs
; US-09-772-772-31

Query Match      88.6%   Score 31: DB 10: Length 6:
Best Local Similarity 83.3%   Pred. No. 5e+05:
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 GRGDTP 6
Db 1 GRGDSP 6

RESULT 14
US-10-262-435-5
; Sequence 5: Application US/0262435
; Publication No. US20030166832A1
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Gideon
```

```

; TITLE OF INVENTION: Methods and Compositions for Impairing
; Multiplication of HIV-1
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Center, P.O. Box 457
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/262.435
; FILING DATE: 30-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/451,067
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/113,921
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: GSP2A/USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-262-435-5

Query Match      88.6%   Score 31: DB 12: Length 6:
Best Local Similarity 83.3%   Pred. No. 5e+05:
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 GRGDTP 6
Db 1 GRGDSP 6

RESULT 15
US-10-325-021-9
; Sequence 9: Application US/10325021
; Publication No. US20030166833A1
; GENERAL INFORMATION:
; APPLICANT: Liolf, Matthias
; APPLICANT: Schense, Jason
; APPLICANT: Hubbell, Jeffery Alan
; APPLICANT: Jen, Anna
; TITLE OF INVENTION: Growth Factor Modified Protein Matrices for Tissue
; FILE REFERENCE: ETH 107 CIP(3)
; CURRENT APPLICATION NUMBER: US/10/325,021
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 10/024,918
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: PCT/EP02/12458
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
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GS-10-325-021-9

Query Match 88.6%; Score 31; DS 12; Length 6;  
Best Local Similarity 81.1%; Pred. No. Se-OS;  
Matches 5; Conservative 1; Mismatches 2; Gaps 0;

QY 1 GRGDIP 6  
III  
Db 1 GRGOSP 6

Search completed: September 16, 2003, 18:21:52  
Job time : 25 sec's

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2003, 18:18:28 : Search time 14 Seconds  
(without alignments)  
41,215 Million cell updates/sec

Title: US-09-780-612A-1

Perfect score: 35

Sequence: 1 GRGCTP 6

Scoring table: BLAST/MSM2  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96,69682 res.dices

Total number of hits satisfying chosen parameters: 316

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR75:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being listed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	18	51.4	6	PT0280	TC heavy chain CRD3 region (clone 4-91B) - human (fragment)
2	17	48.6	5	PT0608	T-cell receptor be
3	17	48.6	5	PT0690	T-cell receptor be
4	17	48.6	6	151434	RR histone - AF16
5	17	48.6	6	PT0630	T-cell receptor be
6	13	37.1	6	PT0514	T-cell receptor be
7	12	34.3	4	SL7255	ribosomal protein
8	12	34.3	4	PT0711	T-cell receptor be
9	12	34.3	5	P20689	photosystem I 13.4
10	12	34.3	5	PT0513	T-cell receptor be
11	12	34.3	5	PT0538	T-cell receptor be
12	12	34.3	5	PT0703	T-cell receptor be
13	12	34.3	5	PT0573	T-cell receptor be
14	12	34.3	5	PT0579	T-cell receptor be
15	12	34.3	6	S75754	ribosomal protein
16	12	34.3	6	PT0629	T-cell receptor be
17	12	34.3	6	PT0511	T-cell receptor be
18	12	34.3	6	PT0504	T-cell receptor be
19	12	34.3	6	PT0687	T-cell receptor be
20	12	34.3	6	PT0652	T-cell receptor be
21	12	34.3	6	PT0587	T-cell receptor be
22	12	34.3	6	PT0568	T-cell receptor be
23	12	34.3	6	PT0709	T-cell receptor be
24	11	31.4	4	ECXAA	antho-ramide near
25	11	31.4	4	A25844	antho-af amide neu
26	11	31.4	4	S47552	ubiquitin - rat
27	11	31.4	5	C23751	spinal cord peptid
28	11	31.4	5	140702	primase - Citrobac
29	11	31.4	5	B31816	20K protein - Rick

30	11	31.4	5	2	S53595	hypothetical prote
31	11	31.4	5	2	D44823	synaposomal-assoc
32	11	31.4	5	2	CS3284	T-cell receptor be
33	11	31.4	5	2	PT0525	T-cell receptor be
34	11	31.4	5	2	PT0553	T-cell receptor be
35	11	31.4	5	2	PT0561	T-cell receptor be
36	11	31.4	5	2	PT0635	T-cell receptor be
37	11	31.4	5	2	PT0700	T-cell receptor be
38	11	31.4	6	2	A63494	antitubercular gly
39	11	31.4	6	2	A45474	epsilon RIIb -
40	11	31.4	6	2	PT0605	T-cell receptor be
41	11	31.4	6	2	PT0619	T-cell receptor be
42	11	31.4	6	2	PT0668	T-cell receptor be
43	11	31.4	6	2	PT0723	T-cell receptor be
44	11	31.4	6	2	A45946	T-cell receptor ga
45	10	28.6	4	2	A53284	T-cell receptor be

## ALIGNMENTS

RESULT 1  
PT0280  
TC heavy chain CRD3 region (clone 4-91B) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #ext\_change 16-Aug-1996  
C:Accession: PT0280  
C:RefSeq: M173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity at  
A:Reference number: PT0222; M173:108337; PM10:1899102  
A:Accession: PT0280  
A:Molecule type: DNA  
A:Residues: 176 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin  
Query Match 51.4%; Score 18; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGCTP 6  
TG 1 GCGSAP 6

RESULT 2  
PT0608  
T-cell receptor beta chain V-D-J region (120-276) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #ext\_change 30-May-1997  
C:Accession: PT0608  
C:RefSeq: M174, 115-124, 1991  
A:Title: Junctional sequences of total T cell receptor beta chains have few N regions  
A:Reference number: PT0509; M174:91277601; PM10:1711556  
A:Accession: PT0608  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <PFE>  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor  
Query Match 48.6%; Score 17; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRG 3  
TG 3 GRG 5

RESULT 3

PT0690  
T-cell receptor beta chain V-D-J region (140-180) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0690  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0690  
A>Status: translation not shown  
A:Molecule type: cDNA  
A:Residues: 1-5 <FE>  
A:Experimental source: day 16 fetal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 48.6%; Score 17; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GDT 5  
DB 3 GDT 5

RESULT 4  
H4 histone - African clawed frog (fragment)  
C:Species: Xoropus laevis (African clawed frog)  
C:Date: 13-Sep-1996 #sequence\_revision 14-Sep-1996 #text\_change 21 Jul 2000  
C:Accession: 151434  
R:Woodland, H.R.; Warminston, J.R.; Ballantyne, J.F.M.; Turner, P.C.  
Nucleic Acids Res. 12, 4939-4959, 1984  
A:Title: Are there major developmentally regulated H4 gene classes in Xoropus?  
A:Reference number: 151391; MUID:84247348; PMID:633660;  
A:Accession: 151434  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-6 <WOO>  
A:Cross-references: GB:K02304; MLD:g214227; PIRN:AAA49738.1; PDB:g555517

Query Match 48.6%; Score 17; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRG 3  
DB 3 GRG 5

RESULT 5  
PT0630  
T-cell receptor beta chain V-D-J region (111-10) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0630  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0630  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FE>  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 48.6%; Score 17; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GDT 5  
DB 3 GDT 5

DB 3 GDT 5

RESULT 6  
PT0514  
T-cell receptor beta chain V-D-J region (100-400) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0514  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0514  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FE>  
A:Experimental source: adult thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 37.1%; Score 13; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e-05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRG 3  
DB 4 GRG 6

RESULT 7  
S17255  
ribosomal protein YRL1, mitochondrial, questionable yeast (Saccharomyces cerevisiae)  
C:Species: Saccharomyces cerevisiae  
A:Variety: strain 07173  
C:Date: 21-Apr-1993 #sequence\_revision 14-Sep-1994 #text\_change 05-May-1997  
C:Accession: S17255  
R:Gromann, L.; Graack, H.R.; Kraft, V.; Chelli, T.; Goldschmidt-Helms, S.; Kitakawa, F.E.S. Lett. 284, 51-56, 1991  
A:Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit fr  
A:Reference number: S17255; MUID:91265106; PMID:2050626  
A:Accession: S17255  
A:Molecule type: protein  
A:Residues: 1-4 <GRG>  
C:Comment: A coding region for this protein could not be identified in the genome of  
C:Genetics:  
A:Genome: nuclear  
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 34.3%; Score 12; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LP 6  
DB 3 LP 4

RESULT 8  
PT0711  
T-cell receptor beta chain V-D-J region (120-20) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0607; PT0674; PT0678; PT0570; PT0711; PT0710  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0607  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-4 <FEI>  
A:Experimental source: newborn thymus, strain BALB/c, 120-2J  
A:Accession: PT0674

A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-4 <FE2>  
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 14C-1G  
A:Accession: P00678  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-4 <FE3>  
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1L  
A:Accession: P00570  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-4 <FE4>  
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 14-1H  
A:Accession: P00711  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-4 <FE5>  
A:Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)  
A:Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 GD 4  
DB 3 GD 4

RESULT 9  
P00589  
Photosystem I 10.4K H1 chain common tobacco (fragment)  
C:Species: Nicotiana tabacum (common tobacco)  
C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
C:Accession: P00689  
R:Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.  
Plant Physiol. 102, 1259-1267, 1993  
A:Title: Molecular heterogeneity of photosystem I, psal, psae, psaf, psah and psal are a  
A:Reference number: P00689  
A:Accession: P00689  
A:Molecule type: protein  
A:Residues: 1-5 <OH0>  
A:Keywords: chloroplast; photosynthesis; photosystem 1; thylakoid

Query Match 34.3%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 GD 4  
DB 3 GD 4

RESULT 10  
P00513  
T-cell receptor beta chain V-D-J region (100-4AL) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: P00513  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: P00509; MUID:91277601; PMID:1711558  
A:Accession: P00513  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: adult thymus, strain BALB/c, clone 100-4AL  
A:Accession: P00606  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE3>

A:Experimental source: newborn thymus, strain BALB/c, clone 120-1S  
A:Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 GD 4  
DB 3 GD 4

RESULT 11  
P00539  
T-cell receptor beta chain V-D-J region (126-1F) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: P00538; P00539; P00603  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
A:Reference number: P00509; MUID:91277601; PMID:1711558  
A:Accession: P00538  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F  
A:Accession: P00539  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE3>  
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1H  
A:Accession: P00603  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: newborn thymus, strain BALB/c, clone 100-2AC  
A:Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 GD 4  
DB 3 GD 4

RESULT 12  
P00703  
T-cell receptor beta chain V-D-J region (145-1F) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: P00703  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
A:Reference number: P00509; MUID:91277601; PMID:1711558  
A:Accession: P00703  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-5 <FE2>  
A:Experimental source: newborn thymus, strain BALB/c  
A:Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 GD 4  
DB 3 GD 4



## RESULT 13

PT0573  
 T-cell receptor beta chain V-D-J region (141-100) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0573  
 R:Feeney, A.J.,  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; M010:9127760.; PMID:1711558  
 A:Accession: PT0573  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-5 <PEP>  
 A:Experimental source: day 19 fetal thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 34.3%; Score 12; DP 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GD 4  
 II  
 Db 3 GD 4

## RESULT 14

PT0679  
 T-cell receptor beta chain V-D-J region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30 May 1997  
 C:Accession: PT0679; PT0708  
 R:Feeney, A.J.,  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; M010:9127760.; PMID:1711558  
 A:Accession: PT0679  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-5 <PEP>  
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-21  
 A:Accession: PT0708  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-5 <PEP2>  
 A:Experimental source: newborn thymus, strain BALB/c, 151-28  
 C:Keywords: T-cell receptor

Query Match 34.3%; Score 12; DP 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GD 4  
 II  
 Db 3 GD 4

## RESULT 15

S78764  
 ribosomal protein Mkp-S23, mitochondria; bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: S78764  
 R:Graack, H.R.,  
 submitted to the Protein Sequence Database, July 1999  
 A:Reference number: S78760  
 A:Accession: S78764  
 A:Molecule type: protein  
 A:Residues: 1-6 <GRA>  
 C:Keywords: mitochondrion  
 F:1-6/Product: ribosomal protein Mkp-S23 (fragment) #status experimental - EAT

Query Match 34.3%; Score 12; DP 2; Length 5;  
 Best Local Similarity 86.7%; Pred. No. 2.9e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DYP 6  
 II  
 Db 4 DKP 6

Search completed: September 16, 2003, 18:20:58  
 Job time: 14 secs

SwissProt version 5.1.6  
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OM protein : protein search, using sw model

Run on: September 15, 2003, 15:17:43 : Search time 11 seconds  
(without alignments)

25.651 Million cell updates/sec

Title: US-09-780-612A-1

Perfect score: 35

Sequence: 1 GRGCTP 6

Scoring table: BLASTUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt41\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	EB	ID	Description
1	15	42.9	4	1	OCPL_OCTM	P56648 octopus min
2	13	37.1	5	1	UXA4_CHLTR	P36055 chlamydia
3	12	34.3	4	1	RM01_YEAS	P45515 saccharomy
4	12	34.3	6	1	TRP1_PSEU	P56414 pseudomonas
5	11	31.4	5	1	DFG1_MOUSE	P36639 mus m.seu
6	9	25.7	4	1	ACHI_LACRU	P35904 achilia in
7	9	25.7	4	1	OCPL_OCTM	P56648 octopus min
8	8	23.9	5	1	THM1_PECOL	P31924 ascherichia
9	8	22.9	6	1	CIF1_MYTE	P33746 mytilus edu
10	7	20.0	3	1	THY1_PIS	P01151 sus scrofa
11	7	20.0	4	1	LCML_PSEPH	P33516 pseudomonas
12	7	20.0	4	1	TRPT_HUMAN	P31358 homo sapien
13	7	20.0	4	1	RPPT_MVTIN	P30435 botriops in
14	7	20.0	5	1	RI13_LITRU	P42099 litorea rub
15	7	20.0	5	1	PAP2_PAPPA	P31864 parichthys
16	7	20.0	5	1	PAC1_PEPAR	P31374 periplaneta
17	7	20.0	5	1	SUGA_ACHDO	P39991 achelia domo
18	7	20.0	5	1	TPIS_CANFA	P34734 canis fami
19	7	20.0	6	1	CIF2_MYTE	P33737 mytilus edu
20	7	20.0	6	1	RI01_LITRU	P32094 litorea rub
21	7	20.0	6	1	FARP_MONEX	P31956 monozia ex
22	7	20.0	6	1	OWA_LEPDE	P42985 lepidopterys
23	7	20.0	6	1	THOF_SARGO	P41495 sarcophaga
24	7	20.0	6	1	V219_HSVIK	P23210 herpes simp
25	6	17.1	3	1	GRWM_HUMAN	P31157 homo sapien
26	6	17.1	3	1	LUXE_VIRPI	P42472 vibrio fisc
27	6	17.1	4	1	EQSI_HUMAN	P32731 homo sapien
28	6	17.1	5	1	AUL4_CANNA	P31817 carcinus ma
29	6	17.1	5	1	BIOA_CITFR	P33071 citrobacter
30	6	17.1	5	1	RE11_LITRU	P32076 litorea rub
31	6	17.1	5	1	RE32_LITRU	P52073 litorea rub
32	6	17.1	6	1	ASP2_LACSN	P42655 lactobacilli
33	6	17.1	6	1	LOK1_LOCMI	P4149: locusta mig

34 6 17.1 6 1 UNO6\_CLOSA  
35 5 14.3 4 1 PAR3\_HIRME  
36 5 14.3 4 1 PAR4\_HIRME  
37 5 14.3 4 1 FLRF\_HIRME  
38 5 14.3 4 1 FERN\_ANFEL  
39 5 14.3 4 1 FWRP\_MACNI  
40 5 14.3 4 1 FYRL\_ANFEL  
41 5 14.3 5 1 FI04\_LITRU  
42 5 14.3 5 1 FARP\_AITFR  
43 5 14.3 5 1 PSK\_DAUCA  
44 5 14.3 5 1 RE31\_LITRU  
45 5 14.3 6 1 ACPH\_RABI

P4135: elostiridium  
P42562 hirudo medi  
P42563 hirudo medi  
P42561 hirudo medi  
P38707 anthopieura  
P0162 macrocallis  
P55706 anthopleura  
P32100 litorea rub  
P41833 artiopesthi  
P382072 caucus caro  
P32072 litorea rub  
P25354 oryctolagus

## ALIGNMENTS

RESULT 1  
OCPL\_OCTM:  
10 OCPL\_OCTM STANDARD; PRI: 4 AA.  
AC P56648:  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cardioactive peptides Ocp-1/Ocp-2.  
OS Octopus minor (Octopus).  
GC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neorolecoidea;  
CC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
OX NCBI\_TaxID=89766;  
RN [1]  
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
RC TISSUE=Brain;  
RX MEDLINE=20336815; PubMed=10876344;  
RA Iwakoshi E., Hisada M., Minakata H.;  
RT Cardioactive peptides isolated from the brain of a Japanese octopus.  
RL Peptides 21:623-630(2000).  
CC FUNCTION: Cardioactive; has both positive chronotropic and  
inotropic effects on the heart. Ocp-2 is a 1000 time less  
active than Ocp-1.  
CC SUBCELLULAR LOCATION: Secreted.  
CC PTM: Ocp-2 has D-phe instead of D-phe.  
CC MASS SPECTROMETRY: MW=495.2; METHOD=MALDI.  
KW Hormone; D-amino acid.  
FT MCD\_RPS 2 2 D-PHENYLALANINE.  
SQ SEQUENCE 4 AA: 394 MW: 6AA879C8160000C0 GR054;  
Query Match 42.9% Score 15; DB 1; Length 4;  
Seqs Local Similarity 75.0%; Pred. No. 13e-05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GRGD 4  
DI 1 1  
DI 1 QFGD 4  
RESULT 2  
UXA4\_CHLTR  
10 UXA4\_CHLTR STANDARD; PRI: 5 AA.  
AC P36055:  
DT 31-OCT-1994 (Rel. 30, Created)  
DT 31-OCT-1994 (Rel. 30, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Unknown protein from 2D-page from elementary body (Fragment).  
OS Chlamydia trachomatis.  
CC Bacteria; Chlamydiae; Chlamydiales; Chlamydiae; Chlamydia.  
CX NCBI\_TaxID=813;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=L2/434/Bu;  
RA Rini L., Santucci A., Maggi B., Marzocchi B., Sanchez-Campillo M.,  
RA Comanducci M., Christianen G., Birkelund S., Viretten E., Ratti G.,  
RA Pallini V.

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      Electrophoresis 15:735-745 (1994).
      -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PT OF THIS UNKNOWN
      CC      PROTEIN IS: 6.6, ITS MW IS: 19 kDa.
      CC      NON_TIER      5
      SQ      SEQUENCE      5 AA; 717 MW; 7364087043100000 CRC64;

      Query Match:      31.4%; Score 11; WP 1; Length 5;
      Best Local Similarity 100.0%; Pred. No. 1.3e+05;
      Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

      QY      1 GR 2
      LL      3 GR 4

      RESULT 6
      ACHI_ACHFU
      ID      ACHI_ACHFU      STANDARD;      PRT;      4 AA.
      AC      F35904;
      DT      01-JUN-1994 (Rel. 29, Created)
      DT      01-JUN-1994 (Rel. 29, Last sequence update)
      DT      15-JUL-1998 (Rel. 36, Last annotation update)
  
```

DE Achatin-1.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stigmatoatopoda;  
OC Sigmurethra; Achatinoidae; Achatinidae; Achatina.  
OX NCBI\_TaxID=6540;  
RN [1]  
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.  
RC STRAIN=FERUSSAC; TISSUE=Ganglion;  
RX MEDLINE=89273551; PubMed=2597281;  
RA Kamatani Y., Minakata H., Ronny P.T.M., Iwashita T., Watanabe K.,  
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Navales-Li P.,  
RA Novalles E.T., Kanapi C.G., Takeuchi H., Nomoto K.,  
RT Achatin-1, an endogenous neuroexcitatory tetrapeptide from Achatina  
RT fulica Ferussac containing a D-amino acid residue.  
RL Biochem. Biophys. Res. Commun. 160:1615-1620(1989).  
RN [2]  
RN CHARACTERIZATION.  
RC STRAIN=FERUSSAC; TISSUE=Heart atrium;  
RX MEDLINE=91264856; PubMed=1675566;  
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
RA Yoshida M., Harada A., Murooka Y., Kobayashi M.,  
RT Purification of achatin-1 from the atria of the African giant snail,  
RT Achatina fulica, and its possible function.  
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).  
RN [3]  
RN X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE=93014529; PubMed=1399265;  
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
RA Iwashita T., Nomoto K.,  
RT Crystal structure and molecular conformation of achatin-1  
RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a  
RT D-amino acid residue.  
RL Int. J. Pept. Protein Res. 45:258-264(1992).  
CC -1- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY  
CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY  
CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE  
CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.  
DR PIR: A32480; A12480.  
KW Hormone; D-amino acid.  
FT MOD\_RES 2 2 D-PHENYLALANINE.  
SQ SEQUENCE 4 AA: 408 MW: 5AADF9E91C009000 CRC64:  
  
Query Match 25.7%; Score 9; DB 1; Length 4;  
Best Local Similarity 59.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 GRGD 4  
DB 1 GPAD 4

RESULT 7  
OCPI\_OCTMI  
ID OCP3\_OCTMI STANDARD; PSI: 4 AA.  
AC P58649;  
DT 28-FEB-2003 (Rel. 41, Created);  
DT 28-FEB-2003 (Rel. 41, Last sequence update);  
DT 28-FEB-2003 (Rel. 41, Last annotation update);  
DE Cardioactive peptides Ocp-3/Ocp-4.  
OS Octopus minor (Octopus).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Colecoidea; Neocoleoidea;  
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
OX NCBI\_TaxID=85766;  
RN [1]  
RN SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
RC TISSUE=Brain;  
RX MEDLINE=20336815; PubMed=10875044;  
RA Iwakoshi E., Hisada M., Minakata H.,  
RT Cardioactive peptides isolated from the brain of a Japanese octopus,  
RT Octopus minor.  
RL Peptides 21:623-630(2000).  
CC -1- FUNCTION: Cardioactive; has both positive chronotropic and  
CC inotropic effects on the heart. Ocp-4 is a 1000 time less

QC active than Ocp-3.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- PTM: Ocp-4 has D-Ser instead of L-Ser.  
CC -1- MASS SPECTROMETRY: MW:95.2; METHOD=MALDI.  
KW Hormone; D-amino acid.  
FT MOD\_RES 2 2 D-SERINE (IN OCP-4)  
SQ SEQUENCE 4 AA: 463 MW: 6AB455B810550000 CRC64:  
  
Query Match 25.7%; Score 9; DB 1; Length 4;  
Best Local Similarity 50.0%; Pred. No. 5.1e+05;  
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 GRGD 4  
DB 1 GSWD 4

RESULT 8  
TRM3\_ECOLI  
ID TRM3\_ECOLI STANDARD; PSI: 5 AA.  
AC P13973;  
DT 01-JAN-1990 (Rel. 13, Created);  
DT 01-JAN-1990 (Rel. 13, Last sequence update);  
DT 28-FEB-2003 (Rel. 41, Last annotation update);  
DE Trm protein (Fragment).  
GN TRAM.  
OS Escherichia coli.  
OC Plasmid IncFII R100.  
CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
CC Enterobacteriaceae; Escherichia.  
CX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88227859; PubMed=2836343;  
RA Imamoto S., Yoshioka Y., Ohtsubo E.,  
RT Identification and characterization of the products from the trm3  
RT and trm genes of plasmid R100.  
RL J. Bacteriol. 170:2749-2757(1988).  
CC -1- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION  
CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE TRAM FAMILY.  
CC  
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC  
DR EXBL: M20941; NOT\_ANNOTATED\_TIS.  
LR PIR: A32014; A32014.  
KW Conjugation; Plasmid; DNA-binding.  
FT MOD\_RES 1 1  
SQ SEQUENCE 5 AA: 634 MW: 6B1B1A4435000000 CRC64:  
  
Query Match 22.9%; Score 8; DB 1; Length 5;  
Best Local Similarity 33.3%; Pred. No. 1.3e+05;  
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 RGD 4  
DB 1 KND 3

RESULT 9  
CIP1\_MYTD  
ID CIP1\_MYTD STANDARD; PSI: 6 AA.  
AC P13736;  
DT 01-JAN-1990 (Rel. 13, Created);  
DT 01-JAN-1990 (Rel. 13, Last sequence update);  
DT 15-DEC-1998 (Rel. 37, Last annotation update);

DE Contraction-inhibiting peptide I (MIP I).  
OS Mytilus edulis (Blue mussel).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;  
OX Mytiloidea; Mytilidae; Mytilus.  
RN NCBI\_TaxID=6250;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Pedal ganglion;  
RX MEDLINE=86240357; PubMed=3377776;  
RA Hirata T., Kubota T., Iwasawa N., Takabatake I., Ikeda T., Murecka Y.:  
RT "Structures and actions of Mytilus inhibitory peptides.";  
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN  
MUSCLES.  
CC -!- SIMILARITY: TO MIP I2.  
DR PIR: A27696; A27696.  
KW Hormone; Amidation.  
FT MOD\_RES 6 AMIDATION.  
SQ SEQUENCE 6 AA: 637 MW: 726968775B81000 CRC64:  
Query Match 22.9%; Score 8; DB 1; Length 6;  
Best Local Similarity 50.0%; Pred. No. 1; Gap 0;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 5 IP 6  
DB 2 SP 3  
RESULT 10  
ID THYL\_PIG STANDARD: PRT: 3 AA.  
AC P01151;  
DT 21-JUL-1986 (Rel. 01, Created)  
DI 21-JUL-1986 (Rel. 01, Last sequence update)  
DE Thyroliberin (thyrotropin releasing hormone) (TRH) (protein).  
OS Sus scrofa (Pig).  
OS Ovis aries (Sheep).  
OS Bombina orientalis (Oriental fire-bellied toad), and  
OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823, 9940, 8346, 8316;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Pig; TISSUE=Hypothalamus;  
RX MEDLINE=70135150; PubMed=4944938;  
RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.:  
RT "Structure of porcine thyrotropin releasing hormone.";  
RL Biochemistry 9:1103-1106(1970).  
RN [2]  
RP SYNTHESIS.  
RC SPECIES=Pig;  
RX MEDLINE=70039904; PubMed=4982117;  
RA Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.:  
RT "The identity of chemical and hormonal properties of the thyrotropin  
releasing hormone and pyroglutaryl-histidyl-proline amide.";  
RL Biochem. Biophys. Res. Commun. 37:705-710(1969).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=Sheep; TISSUE=Hypothalamus;  
RA Desiderio D.M. Jr., Burkus R., Dunn T.F., Vale W., Guillemin R.:  
RT "The elucidation of the primary structure of the hypothalamic thyroid  
stimulating hormone releasing factor of ovine origin by means of mass  
spectrometry.";  
RL Org. Mass Spectrom. 5:221-228(1971).  
RN [4]  
RP SYNTHESIS.  
RC SPECIES=Sheep;  
RX MEDLINE=70163386; PubMed=4965794;  
RA Burkus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.

RA Guillemin R.:  
PT "Characterization of ovine hypothalamic hypophysiotropic  
TSH-releasing factor.";  
RL Nature 226:321-325(1970).  
RN [5]  
RP SEQUENCE.  
RC SPECIES=B orientalis; TISSUE=Skin;  
RX MEDLINE=76138399; PubMed=815011;  
RA Yasuhara T., Nakajima I.:  
RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";  
RL Chem. Pharm. Bull. 23:3301-3303(1975).  
RN [6]  
RP SEQUENCE.  
RC SPECIES=N. viridescens;  
RX MEDLINE=75035605; PubMed=4214528;  
RA Grumm-Joergensen Y., McKelvey J.F.:  
RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus  
viridescens) brain in vitro: Isolation and characterization of  
thyrotropin releasing factor.";  
RL J. Neurochem. 23:471-478(1974).  
CC -!- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH  
IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/  
NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.  
CC -!- SIMILARITY: TO TSH.  
DR PIR: A56919; RHDTG.  
DR PIR: A29711; A92971.  
DR PIR: A33750; RSHST.  
KW Amidation; Pyroglutamate carboxylic acid.  
FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
FT MOD\_RES 3 3 AMIDATION.  
SQ SEQUENCE 3 AA: 380 MW: 776166800000000 CRC64:  
Query Match 20.0%; Score 7; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1; Gap 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 P 6  
DB 3 P 3  
RESULT 11  
ID DCM\_PSECH STANDARD: PPT: 4 AA.  
AC P19916;  
DT 31-FEB-1991 (Rel. 17, Created)  
DI 31-FEB-1991 (Rel. 17, Last sequence update)  
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO  
dehydrogenase subunit L) (CO-DH L) (Fragment).  
GN CUTL  
OS Pseudomonas carboxydohydrogena.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae.  
OX NCBI\_TaxID=290;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=90055678; PubMed=2818128;  
RA Kraat M., Hugendieck J., Herwig S., Meyer O.:  
RT "Homology and distribution of CO dehydrogenase structural genes in  
carboxydohydrogenic bacteria.";  
RL Arch. Microbiol. 152:335-341(1989).  
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
dioxide.  
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced  
acceptor.  
CC -!- COFACTOR: Molybdenum (molybdopterin).  
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND  
SMALL.  
DR PIR: P10140; P10140.  
KW Oxidoreductase; Molybdenum.  
FT NONTER 4 4  
SQ SEQUENCE 4 AA: 441 MW: 776187600000000 CRC64:

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Query Match          20.0%  Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 P 6
DB 4 P 4

RESULT 12
TUFT_HUMAN
ID TUFT_HUMAN STANDARD: PRT: 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phagocytosis-stimulating peptide (Tuftsin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Rodentia; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.
RX MEDLINE=72187087; PubMed=4112769;
RA Nishida K., Constantinopoulos A., Satch P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
stimulating peptide tuftsin.";
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN [2]
RN IMMUNOGLOBULIN CLASS.
RX MEDLINE=72187087; PubMed=4112769;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
effect of leucophilic gamma globulin (leucokinin) on the phagocytic
activity of human polymorphonuclear leucocytes.";
RL Biochemistry 6:3386-3392(1967).
CC -!- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE
CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE
MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
ACTIVITY OF NEUTROPHILS.
DR PIR: A02147; A02147.
DR MM: 191150;
DR GO: GO:0003823; Phagocytosis; NAS.
DR SO: GO:0006509; Phagocytosis; NAS.
SQ SEQUENCE 4 AA: 501 MW: 7417632100000000 CRC64:

Query Match          20.0%  Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 P 6
DB 3 P 3

RESULT 13
BPP7_BOTIN
ID BPP7_BOTIN STANDARD: PRT: 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
enzyme inhibitor).
OS Bothrops insularis (Island Jararaca) (Ocellular Jararaca)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RN SEQUENCE.
RX MEDLINE=90351557; PubMed=2385615;
RA Cintra A.C.O., Vieira C.A., Sgallio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1993).
CC -!- FUNCTION: This peptide both inhibits the activity of the
angiotensin-converting enzyme and enhances the action of
bradykinin by inhibiting the kinases that deactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR: G37196; G37196.
DR KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 5 AA: 629 MW: 7765047326800000 CRC64:

Query Match          20.0%  Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 P 6
DB 5 P 5

RESULT 14
E103_LITRU
ID E103_LITRU STANDARD: PRT: 5 AA.
AC P82059;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RN SEQUENCE.
RX MEDLINE=521639-645(1999);
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian bushy tree frog
Litoria electrica. Comparison with the skin peptides from Litoria
rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA: 630 MW: 6697612090000000 CRC64:

Query Match          20.0%  Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 P 6
DB 4 P 4

RESULT 15
PAP2_PAPMA
ID PAP2_PAPMA STANDARD: PRT: 5 AA.
AC P61864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXL) (Fragment).
OS Pardachirus marmoratus (Red sea mores sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleioidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;

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RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=87057369; PubMed=378233;  
RA Lazarovici P., Primor N., Loew L.M.;  
RI "Purification and pore-forming activity of two hydrophobic  
RT polypeptides from the secretion of the Red sea moses sole (Paralichthys  
RM marmotatus).";  
RL J. Biol. Chem. 261:16704-16713(1986);  
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant  
CC properties. Forms voltage-dependent, ion-permeable channels  
CC in membranes. At high concentration causes cell membrane lysis.  
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE PARAXIN FAMILY.  
KW Toxin.  
FT NON\_TER 5 5  
SQ SEQUENCE 5 AA: 614 MW: 77699030810000 OMC64;

Query Match 20.0%; Score 7; DB 1; Length 5;  
Best Local Similarity 100.0%; Prod No. 1; Gap 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 P 6  
D0 5 P 5

Search completed: September 16, 2003, 18:19:57  
Job time : 12 secs





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3N SEQUENCE.
3P STRAIN=cv, ALVARO; TISSUE=Leaf;
3R MEDLINE=20435798; PubMed=10874046;
3A Yamaguchi K., Subramanian A.R.;
3T "The plastid ribosomal proteins. Identification of all the proteins in
3L the 50 S subunit of an organelle ribosome (chloroplast).";
3R J. Biol. Chem. 275:28466-28482(2000).
3C -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
3C -!- SUBCELLULAR LOCATION: CHLOROPLAST.
3C -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
3C -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 15.5 KDA.
3C -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
3R InterPro: IPR001793; Ribosomal_L10.
3R Pfam: PF00466; Ribosomal_L10; PARTIAL.
3R PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
3R Ribosomal protein; Chloroplast; rRNA-binding.
3T NON_TER 6
3Q SEQUENCE 6 AA: 675 MW; 632184156055E000 CRC64;

Query Match 14.3%; Score 5; DP 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2
DB 4 R 4

RESULT 4
P82541
ID P82541 PRELIMINARY: PRT: 6 AA.
AC P82541
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Chloroplast 36S ribosomal protein S19 beta (fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
NCBI_TaxID=3562;
RN NON_TER 6
SQ SEQUENCE 6 AA: 675 MW; 632184156055E000 CRC64;

SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
STRAIN=cv, ALVARO; TISSUE=Leaf;
MEDLINE=20435797; PubMed=10874033;
Yamaguchi K., von Knoblauch K., Subramanian A.R.;
"The plastid ribosomal proteins. Identification of all the proteins in
the small subunit of an organelle ribosome (chloroplast).";
J. Biol. Chem. 275:28465-28465(2000).
-!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
-!- SUBCELLULAR LOCATION: CHLOROPLAST.
-!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
-!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
-!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
-!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN P1, S19 BETA
FORM IS THE MINOR BASIC FORM.
-!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
-!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro: IPR002222; Ribosomal_S19.
DR Pfam: PF00203; Ribosomal_S19; PARTIAL.
DR PRINTS: PR00975; RIBOSOMALS19; PARTIAL.
DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
T NON_TER 6
SQ SEQUENCE 6 AA: 732 MW; 63333735441C0000 CRC64;

Query Match 14.3%; Score 5; DP 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 I 5
DB 1 I 1

RESULT 5
P82182
ID P82182 PRELIMINARY: PRT: 6 AA.
AC P82182
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 gamma (fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
NCBI_TaxID=3562;
RN NON_TER 6
SQ SEQUENCE 6 AA: 675 MW; 632184156055E000 CRC64;

STRAIN=cv, ALVARO; TISSUE=Leaf;
MEDLINE=20435798; PubMed=10874046;
Yamaguchi K., Subramanian A.R.;
"The plastid ribosomal proteins. Identification of all the proteins in
the 50 S subunit of an organelle ribosome (chloroplast).";
J. Biol. Chem. 275:28466-28482(2000).
-!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
-!- SUBCELLULAR LOCATION: CHLOROPLAST.
-!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
-!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
-!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro: IPR001793; Ribosomal_L10.
DR Pfam: PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
T NON_TER 6
SQ SEQUENCE 6 AA: 675 MW; 632184156055E000 CRC64;

Query Match 14.3%; Score 5; DP 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2
DB 4 R 4

RESULT 6
Q08433
ID Q08433 PRELIMINARY: PRT: 4 AA.
AC Q08433
DT 03-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
RN NON_TER 4
SQ SEQUENCE FROM N.A.
STRAIN=Gunn;
MEDLINE=91282758; PubMed=1840486;
Sato H., Aono S., Kashiwamata S., Kawai O.;
"Genetic defect of bilirubin UDP-glucuronosyltransferase in the
hyperbilirubinemic Gunn rat.";
Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR EMBL: S38636; AAB19259.1; -.
KW Transferase.
T NON_TER 4
SQ SEQUENCE 4 AA: 473 MW; 633732C420000000 CRC64;

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Query Match 5.7% Score 2: 16 11 Length 47  
 Best Local Similarity 0.0% Pred. NO. 8.3e-05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2  
 Db 4 K 4

RESULT 7  
 Q59007 PRELIMINARY: ERT: 5 AA;  
 ID Q99007  
 AC Q99007;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 24, Last annotation update)  
 DE Alpha amylase (Fragment);  
 GN AMY1 GENE;  
 OS Hordeum vulgare (Barley);  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum;  
 CX NCBI\_TaxID=4513;  
 RN [1];  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91329704; PubMed=1531055;  
 RA Jacobsen J.V., Close T.J.;  
 RT "Control of transient expression of chimaeric genes by gibberellic  
 acid and abscisic acid in protoplasts prepared from mature barley  
 aleurone layers.";  
 RL Plant Mol. Biol. 16:713-721(1991).  
 DR EMBL: X54643; CAA38455.1; -;  
 FT NON\_CODING  
 SQ SEQUENCE 5 AA: 60C MW: 51E3344DD6F00000 CRC64;

Query Match 5.7% Score 2: 16 10 Length 5;  
 Best Local Similarity 0.0% Pred. NO. 8.3e-05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2  
 Db 4 K 4

Search completed: September 16, 2003, 18:20:37  
 Job time : 32 secs

16	35	100.0	5	21	AA80475	Cell adhesion pept
17	35	100.0	6	22	AA89742	Fibronectin fragme
18	35	100.0	6	23	AB80076	Integrin modulator
19	35	100.0	9	18	AAK15667	Platelet aggregati
20	35	100.0	9	23	AA61362	Anti-thrombotic cy
21	35	100.0	9	23	AA328644	Integrin-binding p
22	35	100.0	10	18	AAK15655	Platelet aggregati
23	35	100.0	10	18	AAK15656	Platelet aggregati
24	35	100.0	10	18	AAK15657	Platelet aggregati
25	35	100.0	10	18	AAK15658	Platelet aggregati
26	35	100.0	10	18	AAK15659	Platelet aggregati
27	35	100.0	10	18	AAK15663	Platelet aggregati
28	35	100.0	10	18	AAK15672	Platelet aggregati
29	35	100.0	10	23	AB61294	Anti-thrombotic cy
30	35	100.0	10	23	AB61350	Anti-thrombotic cy
31	35	100.0	10	23	AB61351	Anti-thrombotic cy
32	35	100.0	10	23	AB61352	Anti-thrombotic cy
33	35	100.0	10	23	AB61353	Anti-thrombotic cy
34	35	100.0	10	23	AB61354	Anti-thrombotic cy
35	35	100.0	10	23	AB61358	Anti-thrombotic cy
36	35	100.0	10	23	AB61365	Anti-thrombotic cy
37	35	100.0	10	23	AA60330	Human intracellula
38	32	91.4	493	22	AA60330	Human intracellula
39	32	91.4	897	24	AB882571	H. influenzae BASB
40	32	91.4	899	24	AB882572	H. influenzae BASB
41	32	91.4	1005	21	AA601933	Haemophilus influe
42	32	91.4	1011	21	AA601933	Haemophilus influe
43	31	88.6	1012	21	AA601932	Human intracellula
44	31	88.6	1306	22	AA609331	Human intracellula
45	31	88.6	455	21	AA616791	Arabidopsis thalia
46	32	91.4	455	21	AA616791	Arabidopsis thalia
47	32	91.4	458	21	AA616790	Arabidopsis thalia
48	32	91.4	458	21	AA616790	Arabidopsis thalia
49	32	91.4	458	21	AA616790	Arabidopsis thalia
50	32	91.4	1425	22	AB623344	Novel human diagno
51	31	88.6	6	11	AA604612	Antiviral agent.
52	31	88.6	6	11	AA604612	Fibronectin derive
53	31	88.6	6	13	AA606455	Pertig contg. RGD
54	31	88.6	6	13	AA629063	Pertig contg. RGD

RESULT: 1  
AAR36709  
III: AAR36709 standard; peptide: 6 AA.

DE Adhesion formation prevention RGD-contg. peptide.

score greater than or equal to the score of the result being input and is derived by analysis of the total score distribution.

Result No.	Score	Query		DB ID	Description
		Match	Length		
1	35	100.0	6	14	Adhesion formation
2	35	100.0	6	15	PR-30 beta disintegrin
3	35	100.0	6	7	Synthetic peptide
4	35	100.0	6	7	RGD peptide
5	35	100.0	6	20	Neutrophil-activating
6	35	100.0	6	20	Non-cross-linked fibrin
7	35	100.0	6	20	RGD peptide that is
8	35	100.0	6	20	peptide #3 used for
9	35	100.0	6	21	AAR28163



```

RESULT 4
AAR94571
ID AAR94571 standard; Peptide: 6 AA.
XX AC AAR94571:
XX DT 21-JUN-1996 (first entry)
XX DE RGD peptide.
XX KW Cytotactin; neuron; neurite; cell attachment; cell elongation;
XX KW antibody.
XX OS Synthetic.
XX PN W09608513-A1.
XX PD 21-MAR-1996.
XX PF 14-SEP-1995; 95WO-US11684.
XX PR 16-SEP-1994; 94US-C308359.
XX PA (SCR1) SCRIPPS RES INST.
XX PI Crossin KL, Phillips G, Prieto AL;
XX DR WPI; 1995-179904/18.
XX PT Cytotactin polypeptide(s), derivs. and antibodies - capable of
XX PT stimulating neuronal cell attachment, neurite out-growth and cell
XX PT elongation
XX PS Example 5: Page 81; 159pp; English.
XX CC RGD peptides (AAR94570 and AAR94571), inhibitors of cell attachment to
XX CC type I collagen, inhibited attachment of chicken fibroblasts to
XX CC cytotactin (see also AAR94547-48) by 75% and 70% respectively.
XX CC Inhibition was total when the peptides were used together with CG22,
XX CC a function-blocking monoclonal antibody against the beta-1 integrin.
XX CC This suggests that there are 2 integrin binding sites on cytotactin.
XX SQ Sequence 6 AA.
Query Match 100.0%; Score 45; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 5,3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GRGDTP 6
DB 1 GRGDTP 6
RESULT 5
AAY50314
ID AAY50314 standard; Peptide: 6 AA.
XX AC AAY50314:
XX DT 12-JAN-2000 (first entry)
XX DE Neutrophil-activating pancreatic derived peptide 214.
XX KW Cell activation; pancreas; treatment; cardiovascular disease; trauma;
XX KW inflammatory disease; autoimmune diseases; arthritis; diabetes; stroke;
XX KW organ rejection; ischemia; Alzheimer's disease; myocardial infarction;
XX KW haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina;
XX KW trauma; protease inhibitor; hypertension; sepsis.
XX OS Unidentified.
XX PN W09946367-A2.
XX PD
XX PF
XX PR
XX PA
XX PI
XX DR
XX PT
XX PS
XX CC
XX CC RGD peptides (AAR94570 and AAR94571), inhibitors of cell attachment to
XX CC type I collagen, inhibited attachment of chicken fibroblasts to
XX CC cytotactin (see also AAR94547-48) by 75% and 70% respectively.
XX CC Inhibition was total when the peptides were used together with CG22,
XX CC a function-blocking monoclonal antibody against the beta-1 integrin.
XX CC This suggests that there are 2 integrin binding sites on cytotactin.
XX SQ Sequence 6 AA.
Query Match 100.0%; Score 45; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 5,3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GRGDTP 6
DB 1 GRGDTP 6
RESULT 6
AAY31127
ID AAY31127 standard; peptide: 6 AA.
XX AC AAY31127:
XX DT 21-OCT-1999 (first entry)
XX DE Non-crosslinked protein particle peptide 176.
XX KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
XX KW albumin; haemoglobin; nanometer; micrometer; clearance.
XX OS Synthetic.
XX PN
XX PD
XX PF
XX PR
XX PA
XX PI
XX DR
XX PT
XX PS
XX CC
XX CC This invention describes a novel method for the use and preparation of
XX CC cell activating compositions which involves preparing a cell activating
XX CC composition comprising (a) homogenizing pericardiac tissue in buffer at
XX CC about neutral or higher pH to produce a homogenate; (b) removing
XX CC particulates from the homogenate; (c) optionally incubating the
XX CC resulting homogenate, with particulates removed, with a protease; and
XX CC (d) fractionating the homogenate and selecting fractions that exhibit
XX CC cell activation activity. The methods can be used for improving
XX CC treatment outcome or reducing risk of treatment of e.g. cardiovascular
XX CC disease, inflammatory disease, trauma, autoimmune diseases, arthritis,
XX CC organ rejection, diabetes and diabetic complications, stroke, ischemia,
XX CC Alzheimer's disease, myocardial infarction, haemorrhagic shock, diabetic
XX CC retinopathy, diabetes, venous insufficiency, unstable angina or trauma.
XX CC They can be used in the veterinary treatment of a non-human subject.
XX CC Protease inhibitors can be used to lower cell activation resulting from
XX CC these diseases and deficiencies. The detection of an elevated level of
XX CC hydrogen peroxide can be used to detect an inflammatory condition. An
XX CC elevated level of hydrogen peroxide in plasma or whole blood and in the
XX CC presence of superoxide dismutase (SOD) indicates leukocyte up
XX CC regulation, e.g. indicative of the onset of an acute cardiovascular
XX CC disorders, such as disease onset or ischemic complications. An elevated
XX CC level of hydrogen peroxide in plasma or whole blood and a low level in
XX CC the presence of SOD is indicative of a chronic or immune compromised
XX CC condition e.g. hypertension or sepsis. AAY50201-Y50234 represent peptides
XX CC used in the method of the invention.
XX SQ Sequence 6 AA;
Query Match 100.0%; Score 35; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 5,3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GRGDTP 6
DB 1 GRGDTP 6
RESULT 6
AAY31127
ID AAY31127 standard; peptide: 6 AA.
XX AC AAY31127:
XX DT 21-OCT-1999 (first entry)
XX DE Non-crosslinked protein particle peptide 176.
XX KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
XX KW albumin; haemoglobin; nanometer; micrometer; clearance.
XX OS Synthetic.
XX PN
XX PD
XX PF
XX PR
XX PA
XX PI
XX DR
XX PT
XX PS
XX CC
XX CC This invention describes a novel method for the use and preparation of
XX CC cell activating compositions which involves preparing a cell activating
XX CC composition comprising (a) homogenizing pericardiac tissue in buffer at
XX CC about neutral or higher pH to produce a homogenate; (b) removing
XX CC particulates from the homogenate; (c) optionally incubating the
XX CC resulting homogenate, with particulates removed, with a protease; and
XX CC (d) fractionating the homogenate and selecting fractions that exhibit
XX CC cell activation activity. The methods can be used for improving
XX CC treatment outcome or reducing risk of treatment of e.g. cardiovascular
XX CC disease, inflammatory disease, trauma, autoimmune diseases, arthritis,
XX CC organ rejection, diabetes and diabetic complications, stroke, ischemia,
XX CC Alzheimer's disease, myocardial infarction, haemorrhagic shock, diabetic
XX CC retinopathy, diabetes, venous insufficiency, unstable angina or trauma.
XX CC They can be used in the veterinary treatment of a non-human subject.
XX CC Protease inhibitors can be used to lower cell activation resulting from
XX CC these diseases and deficiencies. The detection of an elevated level of
XX CC hydrogen peroxide can be used to detect an inflammatory condition. An
XX CC elevated level of hydrogen peroxide in plasma or whole blood and in the
XX CC presence of superoxide dismutase (SOD) indicates leukocyte up
XX CC regulation, e.g. indicative of the onset of an acute cardiovascular
XX CC disorders, such as disease onset or ischemic complications. An elevated
XX CC level of hydrogen peroxide in plasma or whole blood and a low level in
XX CC the presence of SOD is indicative of a chronic or immune compromised
XX CC condition e.g. hypertension or sepsis. AAY50201-Y50234 represent peptides
XX CC used in the method of the invention.
XX SQ Sequence 6 AA;
Query Match 100.0%; Score 35; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 5,3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GRGDTP 6
DB 1 GRGDTP 6

```

PN US5945033-A.  
 PD 31-AUG-1999.  
 XX 12-NOV-1996; 96US-0747137.  
 XX 14-MAR-1994; 94US-0212546.  
 PR 15-JAN-1991; 91US-0641720.  
 PR 13-OCT-1992; 92US-0959560.  
 PR 01-JUN-1993; 93US-0069831.  
 PR 12-NOV-1996; 96US-0747137.  
 XX (HEMO-) HEMOSPHERE INC.  
 PA Yen RCK;  
 PI WPI: 1999-508153/42.  
 XX Non-crosslinked protein particles for therapeutic and diagnostic use  
 PT Example 22; Column 123-124; 65pp; English.  
 PS This invention describes a novel aqueous suspension of monodisperse  
 CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which  
 CC is stable against dissolving upon dilution with an alcohol-free aqueous  
 CC medium. The method involves (a) forming an aqueous solution containing  
 CC albumin and hemoglobin and (b) treating the aqueous solution with an  
 CC alcohol to cause the solution to become turbid. The particles are useful  
 CC as agents for in vivo administration, either of their own administration  
 CC or as a vehicle for other therapeutic or diagnostic agents. The method  
 CC permits the formation of albumin and hemoglobin particles in the  
 CC nanometer and micrometer size range, in a form closer to their natural  
 CC form than the forms of the prior art. The particles therefore constitute  
 CC a more closely controlled agent for in vivo administration, with greater  
 CC ease of clearance from the body after their period of usefulness.  
 CC AAY30952-Y31135 represent peptides used in the method of the invention.  
 XX Sequence 6 AA:  
 SQ Query Match 100.0%; Score 45; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GKGDTF 6  
 II I I  
 Db 1 GKGDTF 6  
 RESULT 7  
 AAY31025  
 ID AAY31025 standard; peptide: 6 AA.  
 AC AAY31025;  
 XX 21-OCT-1999 (first entry)  
 DT Non-crosslinked protein particle peptide 74.  
 DE Non-crosslinked protein particle; diagnostic; therapy; monodisperse;  
 KW albumin; haemoglobin; nanometer; micrometer; clearance.  
 XX Synthetic.  
 OS US5945033-A.  
 XX 31-AUG-1999.  
 PD 12-NOV-1996; 96US-0747137.  
 XX 14-MAR-1994; 94US-0212546.  
 PR 15-JAN-1991; 91US-0641720.  
 PR 13-OCT-1992; 92US-0959560.  
 PR 01-JUN-1993; 93US-0069831.

PR 12-NOV-1996; 96US-0747137.  
 XX (HEMO-) HEMOSPHERE INC.  
 PA Yen RCK;  
 PI WPI: 1999-508153/42.  
 XX Non-crosslinked protein particles for therapeutic and diagnostic use  
 PT Example 22; Column 81-82; 65pp; English.  
 PS This invention describes a novel aqueous suspension of monodisperse  
 CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which  
 CC is stable against dissolving upon dilution with an alcohol-free aqueous  
 CC medium. The method involves (a) forming an aqueous solution containing  
 CC albumin and hemoglobin and (b) treating the aqueous solution with an  
 CC alcohol to cause the solution to become turbid. The particles are useful  
 CC as agents for in vivo administration, either of their own administration  
 CC or as a vehicle for other therapeutic or diagnostic agents. The method  
 CC permits the formation of albumin and hemoglobin particles in the  
 CC nanometer and micrometer size range, in a form closer to their natural  
 CC form than the forms of the prior art. The particles therefore constitute  
 CC a more closely controlled agent for in vivo administration, with greater  
 CC ease of clearance from the body after their period of usefulness.  
 CC AAY30952-Y31135 represent peptides used in the method of the invention.  
 XX Sequence 6 AA:  
 SQ Query Match 100.0%; Score 45; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GKGDTF 6  
 II I I  
 Db 1 GKGDTF 6  
 RESULT 8  
 AAY84459  
 ID AAY84459 standard; Peptide: 6 AA.  
 AC AAY84459;  
 XX 25-MAR-1999 (first entry)  
 DT RGE peptide that stimulates cell invasion by S. pyogenes 90-226.  
 DE Streptococcus pyogenes 90-226; pathogen; inhibition;  
 KW cell adhesion; cell invasion; treatment; bacterial infection;  
 XX fungal infection.  
 OS Synthetic.  
 XX WO95856408-A2.  
 PN 17-DEC-1998.  
 DE 10-JUN-1998; 98WO-US12019.  
 PF 10-JUN-1997; 97US-0049124.  
 PR (MINU) UNIV MINNESOTA.  
 PA Cleary PP, Cue DR;  
 PI WPI: 1999-080856/07.  
 XX Method for treating mammal infected by pathogenic microorganism -  
 PT comprises administering to mammal composition comprising inhibitory  
 PT compound which inhibits adherence to or invasion of a cell by  
 PT microorganism  
 XX

PS Example 2; Page 43; 83pp; English.

XX The present sequence represents a RGD peptide that is able to  
CC stimulate cell invasion by *Streptococcus pyogenes* 90-226. The  
CC peptides were used in the course of the invention. The  
CC specification describes the treatment of a mammary infected  
CC by a pathogenic microorganism which comprises administering an  
CC inhibitory compound to inhibit adherence to or invasion of cells  
CC by the pathogen. The method is used in the treatment of bacteria,  
CC or fungal infection.

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 23; Length 6;

Best Local Similarity 100.0%; Pred. No. 9; seq 05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6

IIIIII

Db 1 GRGDTP 6

#### RESULT 9

AAB28163  
ID AAB28163 standard; peptide: 6 AA.

AC AAB28163;

XX 09-FEB-2001 (first entry)

XX Peptide #3 used to assay vitronectin receptor binding inhibition.

XX Antiviral; antiinflammatory; cytostatic; vasotropic; antirheumatic;

XX antiarthritic; ophthalmological; osteopathic;

XX amido-carboxylic acid derivative; cancer; angiogenesis;

XX neovascularisation; macular degeneration; glaucoma; blindness

XX rheumatoid arthritis; restenosis; viral infection; bone resorption;

XX osteoporosis; osteopenia; periodontal disease; hyperparathyroidism;

XX Paget's disease; integrin vitronectin receptor; alpha\_vbeta\_3; melanoma.

XX Unidentified.

XX WO200061545-A1.

XX 19-OCT-2000.

XX 13-APR-2000; 2000W-US12027.

XX 14-APR-1999; 9902-0291470.

XX (AMHP ) AMERICAN HOME PROD CORP.

XX Gopalasamy A, Yang HY;

XX WPI: 2000-687029/w7.

XX New amido-carboxylic acid derivatives are integrin inhibitors used for

XX treating e.g. cancer, restenosis, osteoporosis, viral infection and

XX bone disease.

XX Disclosure: Page 17; 67pp; English.

XX The present invention relates to amido-carboxylic acid derivatives. The

XX amido-carboxylic acid derivatives may be used for treating cancer.

XX angiogenesis, neovascularisation, macular degeneration, glaucoma,

XX blindness, rheumatoid arthritis, restenosis, smooth cell proliferation

XX and migration, vascular endothelial cell proliferation and migration.

XX viral infection (characterised by bone resorption of mineralised

XX tissues), osteoporosis, hypercalcaemia of malignancy, osteopenia due to

XX bone metastasis, periodontal disease, hyperparathyroidism, periarthritic

XX erosions in rheumatoid arthritis, Paget's disease, immobilisation-induced

XX osteopenia or glucocorticoid treatment, or diseases characterised by some

XX resorption of mineralised tissues. The present sequence is a peptide.

CC which was used as a reference compound in an assay for the ability of the  
CC amido-carboxylic acid derivatives of the present invention to inhibit  
CC integrin vitronectin receptor (alpha\_vbeta\_3) binding. Integrin  
CC alpha\_vbeta\_3 has been shown to mediate the invasion of carcercous  
CC melanoma cells into healthy tissue and to protect these cells against  
CC apoptosis. In addition, vitronectin receptor antagonists have been shown  
CC to inhibit the growth of various solid tumours of human origin.

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 23; Length 6;

Best Local Similarity 100.0%; Pred. No. 9; seq 05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6

IIIIII

Db 1 GRGDTP 6

#### RESULT 10

AAY80475

ID AAY80475 standard; peptide: 6 AA.

AC AAY80475;

XX 06-JUN-2000 (first entry)

XX Cell adhesion peptide #10.

XX Bone regenerative; osteopathic; osseous tissue; reconstitution;

XX scaffold matrix; bone formation promoter; bone resorption inhibitor;

XX cell adhesion; osteoblast; osteoclast; bone defect; fracture.

XX Synthetic.

XX WO2000004941-A1.

XX 03-FEB-2000.

XX 22-JUL-1999; 99WO-US16803.

XX 24-JUL-1998; 98US-0122348.

XX (PEAR-) PHARMACAL BIOTECHNOLOGIES INC.

XX Budny JA;

XX WPI: 2000-195084/17.

XX System for reconstructing osseous tissue, useful e.g. for treating

XX fractures, comprises scaffold containing promoter of bone formation and

XX inhibitor of bone resorption.

XX Claim 14; Page 31; 44pp; English.

XX The invention relates to a novel system for reconstitution of osseous

XX tissue comprising a scaffold carrying a compound (I) that promotes

XX bone formation and a component that decreases bone resorption (II).

XX (I) induces migration and adhesion of osteoblasts and osteoclasts and

XX (II) inhibits proteolysis (specifically by plasmin) of extracellular

XX matrix. (I) is preferably selected from: secretin or secretin binding

XX fragments, proteins and peptides that facilitate cell adhesion,

XX plasminogen activator inhibitors, protease inhibitors and

XX metalloprotease inhibitors. The peptides AAY80466-Y80492 are claimed

XX examples of cell adhesion peptides used in the system of the invention.

XX The system is used to replace, remodel or correct bone defects, e.g.

XX fractures, fissures or bone mass loss. Incorporation of (I) into the

XX scaffold results in rapid seeding by osteoblasts and the development of

XX an organic matrix, i.e. the preformed scaffold replaces the

XX rate-determining step of extracellular matrix formation. The scaffold can

XX be designed to have a predetermined resorption/degradation rate, and may

XX include regulatory compounds for specific cell types.







XX Integrin-binding peptide.  
DE  
XX  
XX Embolisation therapy; angiogenic-dependant diseases; cancer;  
KW drug delivery; vaccine; microsphere; precancerous; therapeutic factor;  
KW integrin-binding; cytostatic.  
XX  
OS Unidentified.  
XX  
XX WO200172281-A2.  
PN  
XX  
XX 04-OCI-2001.  
PD  
XX  
XX 23-MAR-2001; 2001WO-US05619.  
PF  
XX  
XX 24-MAR-2000; 2000US-191899P.  
PR  
XX  
XX (BIOS-) BIOSPHERE MEDICAL INC.  
PA  
XX  
XX Vogel J, Boschetti E;  
PI  
XX  
XX WPI; 2002-034141/04.  
DR  
XX  
XX Microspheres for active embolisation comprising a cross linked  
PT hydrophilic polymer and a drug or vaccine are useful for site-directed  
PT therapy via the blood supply, particularly of tumours -  
XX  
XX Disclosure; Page 34; 73pp; English.  
PS  
XX  
XX The invention relates to a microsphere suitable for active embolisation,  
CC comprising a biocompatible, cross-linked and substantially hydrophilic  
CC polymer and a drug or vaccine, the activity of which may be described as  
CC cytostatic. Compositions and methods of the invention may be used in the  
CC treatment of angiogenic-dependant diseases including cancer and  
CC precancerous disorders. The microspheres are used for site directed  
CC delivery of therapeutic drugs, pharmaceuticals or vaccines, particularly  
CC for treatment of tumours. The current sequence represents an increase in  
CC binding peptide that may be used as a transfection agent to increase the  
CC efficiency of transfer of a bioactive therapeutic factor into cells.  
XX  
XX  
50 Sequence 9 AA:

Query Match 100.0%; Score 45; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.4e-06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GRGDTP 5  
Db 4 GRGDTP 9  
11111

Search completed: September 16, 2003, 14:15:41  
Job time : 42 secs

Genome version 5.1.6  
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OM protein - Protein search, using sw model

Run on: September 16, 2003, 18:15:57 : Search time 16 seconds  
(without alignments)  
15,467 Million cells updated/sec

Title: US-09-780-612A-1

Perfect score: 35  
Sequence: 1 GRGDTP 6

Scoring table: PLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310859 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 9

Maximum DB seq length: 2090000000

Post-processing: Minimum Match on  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_patents\_AA:\*

- 1: /cgn2.6/plodata/1/aa/7A\_COMB.pep:\*
- 2: /cgn2.6/plodata/1/aa/7B\_COMB.pep:\*
- 3: /cgn2.6/plodata/1/aa/6A\_COMB.pep:\*
- 4: /cgn2.6/plodata/1/aa/6B\_COMB.pep:\*
- 5: /cgn2.6/plodata/1/aa/PCIS\_COMB.pep:\*
- 6: /cgn2.6/plodata/1/aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB ID	Description
		Match	Length		
1	35	100.0	6	1 US-08-169-743-2	Sequence 2, Appl
2	35	100.0	6	1 US-08-178-482-7	Sequence 7, Appl
3	35	100.0	6	1 US-08-234-597-1	Sequence 1, Appl
4	35	100.0	6	2 US-08-747-137-74	Sequence 74, Appl
5	35	100.0	6	2 US-08-747-137-176	Sequence 176, Appl
6	35	100.0	6	3 US-08-956-699-1	Sequence 1, Appl
7	35	100.0	6	4 US-09-606-673-1	Sequence 1, Appl
8	35	100.0	6	4 US-03-485-653-1	Sequence 1, Appl
9	35	100.0	6	4 US-09-548-697A-2	Sequence 2, Appl
10	35	100.0	6	5 PC-US33-05640-45	Sequence 45, Appl
11	35	100.0	9	4 US-08-445-745-114	Sequence 114, Appl
12	35	100.0	9	4 US-08-456-745-92	Sequence 92, Appl
13	35	100.0	9	4 US-08-445-638-114	Sequence 114, Appl
14	35	100.0	10	1 US-08-445-745-50	Sequence 50, Appl
15	35	100.0	10	1 US-08-445-745-51	Sequence 51, Appl
16	35	100.0	10	1 US-08-445-745-102	Sequence 102, Appl
17	35	100.0	10	1 US-08-445-745-103	Sequence 103, Appl
18	35	100.0	10	1 US-08-445-745-104	Sequence 104, Appl
19	35	100.0	10	1 US-08-445-745-105	Sequence 105, Appl
20	35	100.0	10	1 US-08-445-745-106	Sequence 106, Appl
21	35	100.0	10	1 US-08-445-745-110	Sequence 110, Appl
22	35	100.0	10	1 US-08-445-745-117	Sequence 117, Appl
23	35	100.0	10	4 US-08-456-466-24	Sequence 24, Appl
24	35	100.0	10	4 US-08-456-466-80	Sequence 80, Appl
25	35	100.0	10	4 US-08-456-466-81	Sequence 81, Appl
26	35	100.0	10	4 US-08-456-466-82	Sequence 82, Appl
27	35	100.0	10	4 US-08-456-466-83	Sequence 83, Appl

Sequence 84, Appl  
Sequence 88, Appl  
Sequence 95, Appl  
Sequence 50, Appl  
Sequence 51, Appl  
Sequence 102, Appl  
Sequence 103, Appl  
Sequence 104, Appl  
Sequence 105, Appl  
Sequence 106, Appl  
Sequence 110, Appl  
Sequence 117, Appl  
Sequence 12, Appl  
Sequence 41, Appl  
Sequence 39, Appl  
Sequence 13, Appl  
Sequence 46, Appl  
Sequence 5, Appl

ALIGNMENTS

RESULT 1  
US-08-169-743-2  
: Sequence 2, Application US/08.69743  
: Patent No. 5547936  
: GENERAL INFORMATION:  
: APPLICANT: ROUSLAHTI, ERKKI I.  
: APPLICANT: PIERSCHBACHER, MICHAEL D.  
: APPLICANT: GEHLSSEN, KURT R.  
: TITLE OF INVENTION: INHIBITION OF CRIM. MIGRATION WITH  
: TITLE OF INVENTION: SYNTHETIC PEPTIDES  
: NUMBER OF SEQUENCES: 6  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: PRETTY, SCHROEDER, KRUEGGEMANN & CLARK  
: STREET: 444 SOUTH FLOWER STREET, SUITE 2000  
: CITY: LOS ANGELES  
: STATE: CALIFORNIA  
: COUNTRY: UNITED STATES  
: ZIP: 90071  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/169,743  
: FILING DATE:  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/773,106  
: FILING DATE: 08-OCT-1991  
: ATTORNEY/AGENT INFORMATION:  
: NAME: BROWN, THERESA A.  
: REGISTRATION NUMBER: 32,547  
: REFERENCE/DOCKET NUMBER: P319102  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 619-535-9001  
: TELEFAX: 619-535-9949  
: INFORMATION FOR SEQ ID NO: 2:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 6 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
US-08-169-743-2

Query Match 100.0%, Score 35, DB 1, Length 6

Best Local Similarity 100.0%, Pred. No. 2.5e+05, Indels 0, Gaps 0, Mismatches 0

QY 1 GRGDTP 6

|||||

Db 1 GRGDTF 6

```

RESULT 2
US-08-178-482-7
: Sequence 7, Application US/06178462
: Patent No. 5629294
: GENERAL INFORMATION:
: APPLICANT: DIERCKA, GREG S
: APPLICANT: ROGERS, KATHLEEN E
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PREVENTING
: TITLE OF INVENTION: ADHESION FORMATION
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ROBBINS, DALGARN, BEELINER & CARSON
: STREET: 201 NORTH FIGUEROA STREET, FIFTH FLOOR
: CITY: LOS ANGELES
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 90012-2628
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/178,482
: FILING DATE: 06-JAN-1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/759,211
: FILING DATE: 07-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: SPITALS, JOHN P
: REGISTRATION NUMBER: 23,215
: REFERENCE/DOCKET NUMBER: 2520-314
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 977-1001
: TELEFAX: (213) 977-1003
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-178-482-7

Query Match 100.0% Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2,5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRGDTF 6
Db 1 GRGDTF 6

RESULT 3
US-08-234-997-1
: Sequence 1, Application US/08234997
: Patent No. 5684867
: GENERAL INFORMATION:
: APPLICANT: SUMEDHA JAYASRNA
: APPLICANT: GREG BIESECKER
: APPLICANT: LARRY GOLD
: APPLICANT: DREW SMITH
: APPLICANT: GARY KARSCHENHEUTER
: TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
: TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: BLENDED
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Beaton & Swanson, P.C.
: STREET: 4582 South Ulster Street Parkway, #403
: CITY: Denver

```

```

STATE: Colorado
COUNTRY: USA
ZIP: 80237
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,997
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: JUNE 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: JUNE 11, 1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: SEPTEMBER 8, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,935
FILING DATE: SEPTEMBER 17, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/199,507
FILING DATE: FEBRUARY 22, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-3900
TELEFAX: (303) 850-9451
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-234-997-1

Query Match 100.0% Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2,5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRGDTF 6
Db 1 GRGDTF 6

RESULT 4
US-08-747-537-74
: Sequence 74, Application US/08747137
: Patent No. 5945033
: GENERAL INFORMATION:
: APPLICANT: YEN, Richard C.K.
: TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
: TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
: NUMBER OF SEQUENCES: 184
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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? APPLICATION NUMBER: US 08/747,137
? FILING DATE: 12-NOV-1996
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/212,546
? FILING DATE: 14-MAR-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/069,831
? FILING DATE: 01-JUN-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/959,560
? FILING DATE: 13-OCT-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/641,720
? FILING DATE: 15-JAN-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Apple, Randolph T.
? REGISTRATION NUMBER: 36,429
? REFERENCE/DOCKET NUMBER: 016197-000840918
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-576-0200
? INFORMATION FOR SEQ ID NO: 74:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 6 amino acids
? TYPE: amino acid
? STRANDEDNESS: not relevant
? TOPOLOGY: not relevant
US-08-747-137-74

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6
DB 1 GRGTP 6

RESULT 5
US-08-747-137-176
? Sequence 176, Application: US/08747137
? Patent No. 5945011
? GENERAL INFORMATION:
? APPLICANT: YEN, Richard C.K.
? TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
? THERAPEUTIC AND DIAGNOSTIC USE
? NUMBER OF SEQUENCES: 184
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend and Crow LLP
? STREET: Two Embarcadero Center, 8th Floor
? CITY: San Francisco
? STATE: CA
? COUNTRY: USA
? ZIP: 94111
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent's Release #1.0, Version #1.31
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/747,137
? FILING DATE: 12-NOV-1996
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/212,546
? FILING DATE: 14-MAR-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/069,831
? FILING DATE: 01-JUN-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/959,560
? FILING DATE: 13-OCT-1992
? PRIOR APPLICATION DATA:

```

```

? APPLICATION NUMBER: US 07/641,720
? FILING DATE: 15-JAN-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Apple, Randolph T.
? REGISTRATION NUMBER: 36,429
? REFERENCE/DOCKET NUMBER: 016197-000840918
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-576-0200
? INFORMATION FOR SEQ ID NO: 176:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 6 amino acids
? TYPE: amino acid
? STRANDEDNESS: not relevant
? TOPOLOGY: not relevant
US-08-747-137-176

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6
DB 1 GRGTP 6

RESULT 6
US-08-956-699-1
? Sequence 1, Application: US/08956699
? Patent No. 6085696
? GENERAL INFORMATION:
? APPLICANT: GREG BIESECKER
? APPLICANT: SUMEDHA D. JAYASENA
? APPLICANT: LARRY GOLD
? APPLICANT: DREW SMITH
? APPLICANT: GARY P. KINSCHENHEUTER
? TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS
? TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: BLINDED
? NUMBER OF SEQUENCES: 5
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Swanson & Bratschen, L.L.C.
? STREET: 8400 E. Prentice Avenue, Suite 100
? CITY: Englewood
? STATE: Colorado
? COUNTRY: USA
? ZIP: 80111
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: MS-DOS
? SOFTWARE: WordPerfect 6.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/956,699
? FILING DATE: OCTOBER 23, 1997
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/234,997
? FILING DATE: APRIL 28, 1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/714,131
? FILING DATE: JUNE 10, 1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/536,428
? FILING DATE: JUNE 11, 1990
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/117,991
? FILING DATE: SEPTEMBER 8, 1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/123,935
? FILING DATE: SEPTEMBER 17, 1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/199,507
? FILING DATE: FEBRUARY 22, 1994

```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX15/C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3433
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-956-699-1
;
; Query Match 100.0%; Score 35; DB 3; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e-05;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 GRGDTp 6
; Db 1 GRGDTp 6
;
; RESULT 7
; US-09-606-477-1
; Sequence 1, Application US/0960477
; Patent No. 6465189
; GENERAL INFORMATION:
; APPLICANT: GREG RIESECKER
; LARRY GOLD
; SUMEDHA D. CATASANA
; DREW SMITH
; GARY P. KIRSCHENHEUER
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; EXPONENTIAL ENRICHMENT: BLANDED
; SELEX
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 1745 Shea Center Drive, Suite 350
; CITY: Highlands Ranch
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80129
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/606,477
; FILING DATE: 29-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,699
; FILING DATE: OCTOBER 23, 1997
; APPLICATION NUMBER: 08/254,997
; FILING DATE: APRIL 28, 1994
; APPLICATION NUMBER: 07/724,133
; FILING DATE: JUNE 10, 1991
; APPLICATION NUMBER: 07/536,428
; FILING DATE: JUNE 11, 1990
; APPLICATION NUMBER: 08/117,991
; FILING DATE: SEPTEMBER 6, 1993
; APPLICATION NUMBER: 08/23,935
; FILING DATE: SEPTEMBER 17, 1993
; APPLICATION NUMBER: 08/199,507
; FILING DATE: FEBRUARY 22, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX15/C-CON

```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3433
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-606-477-1
;
; Query Match 100.0%; Score 35; DB 4; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e-05;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 GRGDTp 6
; Db 1 GRGDTp 6
;
; RESULT 8
; US-09-485-653-1
; Sequence 1, Application US/09485653
; Patent No. 6555321
; GENERAL INFORMATION:
; APPLICANT: Daniel, Thomas O.
; APPLICANT: Stein, Elke
; TITLE OF INVENTION: Methods for Determining Cell Responses
; TITLE OF INVENTION: Through FcHR Receptors
; FILE REFERENCE: 22000.008501
; CURRENT APPLICATION NUMBER: US/09/485,653
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/US98/17157
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: 60/056,164
; PRIOR FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: FRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6555321e -
; OTHER INFORMATION: Synthetic construct
; US-09-485-653-1
;
; Query Match 100.0%; Score 35; DB 4; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e-05;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 GRGDTp 6
; Db 1 GRGDTp 6
;
; RESULT 9
; US-09-548-697A-2
; Sequence 2, Application US/09548697A
; Patent No. 6586187
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company
; APPLICANT: Gopalsamy, Arinamala
; APPLICANT: Yang, Hui Y
; TITLE OF INVENTION: Methods for Solid Phase Combinatorial Synthesis of Integrin in
; FILE REFERENCE: AHP-98202
; CURRENT APPLICATION NUMBER: US/09/548,697A
; CURRENT FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/240,952
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-548-697A-2

Query Match          100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRGDTTP 6
DB      1 GRGDTTP 6

RESULT 10
PCT-US93-05640-45
; Sequence 45, Application PCT/US93/05640
; GENERAL INFORMATION:
; APPLICANT: University of Connecticut
; TITLE OF INVENTION: Contraceptive Vaccine
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millis Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05640
; FILING DATE: 19930610
; CLASSIFICATION:
; APPLICATION DATA:
; FILING DATE: 07/897,983
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: GC90-01AA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-05640-45

Query Match          100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRGDTTP 6
DB      1 GRGDTTP 6

RESULT 11
US-08-445-745-114
; Sequence 114, Application US/08/445745
; Patent No. 5672585
; GENERAL INFORMATION:
; APPLICANT: Pierschbacher, Michael D.
; Lukeman, David S.
; Cheng, Soan
; Craig, William S.

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; APPLICANT: Pierschbacher, Michael D.
; APPLICANT: Cheng, Soan
; APPLICANT: Craig, William S.
; APPLICANT: Tschoop, Juerg F.
; TITLE OF INVENTION: Methods and Composition for Treating
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,745
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,064
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: US 08/079,441
; FILING DATE: 18-JUN-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,736/4
; FILING DATE: 14-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,119
; FILING DATE: 05-APR-1991
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/506,444
; FILING DATE: 06-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9825
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note="Xaa" = {Imp}"
US-08-445-745-114

Query Match          100.0%; Score 35; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRGDTTP 6
DB      2 GRGDTTP 7

RESULT 12
US-08-456-466-92
; Sequence 92, Application US/08/456466
; Patent No. 6395873
; GENERAL INFORMATION:
; APPLICANT: Pierschbacher, Michael D.
; Lukeman, David S.
; Cheng, Soan
; Craig, William S.

```

Tschopp, Juerg F.  
TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATING  
THROMBOSIS

NUMBER OF SEQUENCES: 120  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: CAMPBELL & FLORES, LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/02/456,466

FILING DATE: 01-JUN-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION/DOCKET NUMBER: P-1A 1537

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 92:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: circular

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note- "Xaa-Pmp"

SEQUENCE DESCRIPTION: SEQ ID NO: 92:

S-08-456-466-92

Query Match 100.0%; Score 35; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GRGDIP 6

||||

D 2 GRGDIP 7

# RESULT 13

S-08-445-638-114

Sequence 114, Application: US/08445638

Patent No. 6521594

GENERAL INFORMATION:

APPLICANT: Pierschbacher, Michael D.

APPLICANT: Cheng, Soan

APPLICANT: Craig, William S.

APPLICANT: Tschopp, Juerg F.

TITLE OF INVENTION: Methods and Composition for Treating

THROMBOSIS

NUMBER OF SEQUENCES: 168

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/445,638

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/471,668

FILING DATE: 20-DEC-1993

APPLICATION NUMBER: US 08/079,411

FILING DATE: 18-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/050,736/14

FILING DATE: 14-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/681,119

FILING DATE: 05-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/506,444

FILING DATE: 06-APR-1990

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION/DOCKET NUMBER: P-1A 9829

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 114:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: circular

FEATURE:

NAME/KEY: Peptide

LOCATION: 1

OTHER INFORMATION: /note- "Xaa - {Pmp}"

S-08-445-638-114

Query Match 100.0%; Score 35; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GRGDIP 6

||||

D 2 GRGDIP 7

# RESULT 14

S-08-445-745-50

Sequence 50, Application: US/08445745

Patent No. 5672585

GENERAL INFORMATION:

APPLICANT: Pierschbacher, Michael D.

APPLICANT: Cheng, Soan

APPLICANT: Craig, William S.

APPLICANT: Tschopp, Juerg F.

TITLE OF INVENTION: Methods and Composition for Treating

THROMBOSIS

NUMBER OF SEQUENCES: 168

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/445,745

FILING DATE:

CLASSIFICATION: 514



```

1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: US 06/171,068
3 FILING DATE: 20-DEC-1993
4 APPLICATION NUMBER: US 06/079,441
5 FILING DATE: 18-JUN-1993
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: US 06/050,745
8 FILING DATE: 14-APR-1993
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 07/681,119
11 FILING DATE: 05-APR-1991
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US 07/506,444
14 FILING DATE: 06-APR-1990
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 07/506,444
17 FILING DATE: 06-APR-1990
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Campbell, Cathryn A.
20 REGISTRATION NUMBER: 31,815
21 REFERENCE/DOCKET NUMBER: P-1A 9829
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: (619) 535-9061
24 TELEFAX: (619) 535-8949
25 INFORMATION FOR SEQ ID NO: 50:
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 10 amino acids
28 TYPE: amino acid
29 TOPOLOGY: circular
30 FEATURE:
31 NAME/KEY: Peptide
32 LOCATION: 2
33 OTHER INFORMATION: /note: "Xaa = (Leu)"
34 US-08-445-745-50

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Query Match 100.0% Score 45: DB 1: Length 10:
Best Local Similarity 100.0% Pred. No. 0.75:
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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QY 1 GRGDTP 6
DB 3 GRGDIP 8

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RESULT 15
US-08-445-745-51
: Sequence 51, Application US/08445745
: Patent No. 5672585
: GENERAL INFORMATION:
: APPLICANT: Pierschbacher, Michael D.
: APPLICANT: Cheng, Sean
: APPLICANT: Craig, William S.
: TITLE OF INVENTION: Methods and Composition for Treating
: TITLE OF INVENTION: Thrombosis
: NUMBER OF SEQUENCES: 168
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell and Flores
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/445,745
: FILING DATE:
: CLASSIFICATION: 5.14
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 06/171,068
: FILING DATE: 20-DEC-1993
: APPLICATION NUMBER: US 06/079,441

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1 FILING DATE: 18-JUN-1993
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: US 08/050,745
4 FILING DATE: 14-APR-1993
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US 07/681,119
7 FILING DATE: 05-APR-1991
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: US 07/506,444
10 FILING DATE: 06-APR-1990
11 ATTORNEY/AGENT INFORMATION:
12 NAME: Campbell, Cathryn A.
13 REGISTRATION NUMBER: 31,815
14 REFERENCE/DOCKET NUMBER: P-1A 9829
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (619) 535-9061
17 TELEFAX: (619) 535-8949
18 INFORMATION FOR SEQ ID NO: 51:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 10 amino acids
21 TYPE: amino acid
22 TOPOLOGY: circular
23 FEATURE:
24 NAME/KEY: Peptide
25 LOCATION: 2
26 OTHER INFORMATION: /note: "Xaa = (Leu)"
27 US 08-445-745-51

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Query Match 100.0% Score 45: DB 1: Length 10:
Best Local Similarity 100.0% Pred. No. 0.75:
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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QY 1 GRGDTP 6
DB 3 GRGDIP 8

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Search completed: September 16, 2003, 18:18:24
Job time : 17 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM protein - protein search, using sw mode:

Run on: September 16, 2003, 16:16:48 : Search time 26 seconds  
(without alignments)  
34,360 Million cell updates/sec

Title: US-09-780-612A-1

Perfect score: 35

Sequence: 1 GRGDTTP 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 556269 seqs, 148843469 residues  
Total number of hits satisfying chosen parameters: 65269

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications, AA:  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:  
2: /cgn2\_6/ptodata/2/pubpaa/PCR\_NEW\_PUB.pep:  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:  
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7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:  
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9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:  
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14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	12	US-10-420-029-1
2	35	100.0	6	14	US-10-027-270-33
3	35	100.0	6	15	US-10-263-456-1
4	35	100.0	1005	12	US-10-193-764-41
5	35	100.0	1005	12	US-10-193-764-39
6	32	91.4	1517	15	US-10-156-761-13265
7	31	88.6	6	9	US-09-837-969A-28
8	31	88.6	6	9	US-09-837-969A-46
9	31	88.6	6	9	US-09-837-969A-15
10	31	88.6	6	9	US-09-837-969A-1
11	31	88.6	6	10	US-09-364-597A-21
12	31	88.6	6	10	US-09-177-643-1
13	31	88.6	6	10	US-09-841-321A-26
14	31	88.6	6	10	US-09-841-321A-46
15	31	88.6	6	10	US-09-871-574-3

16	31	88.6	6	10	US-09-972-772-31	Sequence 31, Appl
17	31	88.6	6	12	US-10-262-445-5	Sequence 5, Appl
18	31	88.6	6	12	US-10-325-027-9	Sequence 9, Appl
19	31	88.6	6	14	US-10-021-945-31	Sequence 3, Appl
20	31	88.6	6	14	US-10-027-270-32	Sequence 32, Appl
21	31	88.6	6	14	US-10-027-270-35	Sequence 35, Appl
22	31	88.6	6	14	US-10-114-176-2	Sequence 2, Appl
23	31	88.6	6	15	US-10-046-801-5	Sequence 5, Appl
24	31	88.6	6	15	US-10-247-850-83	Sequence 83, Appl
25	31	88.6	6	15	US-10-138-935-4	Sequence 31, Appl
26	31	88.6	7	8	US-08-987-756-1	Sequence 1, Appl
27	31	88.6	7	10	US-05-364-537A-22	Sequence 22, Appl
28	31	88.6	7	11	US-05-911-569-8	Sequence 8, Appl
29	31	88.6	7	12	US-10-200-579-8	Sequence 8, Appl
30	31	88.6	7	12	US-10-420-029-1	Sequence 3, Appl
31	31	88.6	8	9	US-05-096-743A-96	Sequence 96, Appl
32	31	88.6	8	9	US-09-892-071-3	Sequence 3, Appl
33	31	88.6	8	10	US-09-753-126-6	Sequence 6, Appl
34	31	88.6	8	11	US-05-903-412-96	Sequence 96, Appl
35	31	88.6	8	12	US-10-165-165-96	Sequence 96, Appl
36	31	88.6	8	13	US-10-190-192-96	Sequence 96, Appl
37	31	88.6	8	15	US-10-174-717A-94	Sequence 11, Appl
38	31	88.6	9	9	US-09-892-071-1	Sequence 1, Appl
39	31	88.6	10	9	US-09-809-252-3	Sequence 1, Appl
40	31	88.6	10	9	US-09-892-071-1	Sequence 1, Appl
41	31	88.6	10	9	US-05-892-071-8	Sequence 8, Appl
42	31	88.6	10	14	US-10-007-270-16	Sequence 36, Appl
43	31	88.6	10	14	US-10-007-270-37	Sequence 37, Appl
44	31	88.6	11	9	US-09-837-969A-21	Sequence 11, Appl
45	31	88.6	11	10	US-09-841-321A-11	Sequence 11, Appl

## ALIGNMENTS

RESULT 1  
US-10-420-029-1  
Sequence 1, Application US/10420029  
Publication No. US20030157712A1  
GENERAL INFORMATION:  
APPLICANT: Daniel, Thomas C.  
APPLICANT: Stein, Elke  
TITLE OF INVENTION: Methods for Determining Cell Responses  
TITLE OF INVENTION: Through EphA Receptors  
FILE REFERENCE: 22000.008502  
CURRENT APPLICATION NUMBER: US/10/420.029  
CURRENT FILING DATE: 2003-04-17  
PRIOR APPLICATION NUMBER: 09/485,653  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: PCT/US98/17157  
PRIOR FILING DATE: 1998-08-19  
PRIOR APPLICATION NUMBER: 60/056,164  
PRIOR FILING DATE: 1997-08-19  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: No. US20030157712A1e -  
OTHER INFORMATION: Synthetic construct  
US-10-420-029-1

Query Match 100.0% Score 35: DB 12: Length 6:  
Best Local Similarity 100.0% Pred. No. 5e+05:  
Matches 6: Conservative 0: Mismatches 0: Intels 0: Gaps 0:

QY 1 GRGDTTP 6

26 1 GRGDTTP 6

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RESULT 2
US-10-007-270-33
: Sequence 33, Application US/10-07270
: Publication No. US20020143954A1
: GENERAL INFORMATION:
: APPLICANT: Kuehn, Markus H.
: APPLICANT: Kuehn, Markus H.
: APPLICANT: University of Iowa Research Foundation
: TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
: FILE REFERENCE: 025618 000127US
: CURRENT APPLICATION NUMBER: US/10/007,270
: PRIOR FILING DATE: 2001-11-08
: PRIOR APPLICATION NUMBER: US 09/430,195
: PRIOR FILING DATE: 1999-10-29
: PRIOR APPLICATION NUMBER: US 09/183,972
: PRIOR FILING DATE: 1998-10-29
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 33
: LENGTH: 6
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:
: OTHER INFORMATION: RGD-containing peptide
US-10-007-270-33

Query Match          100.0%; Score 35; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTTP 6
DB 1 GRGDTTP 6

RESULT 3
US-10-263-456-1
: Sequence 1, Application US/10263456
: Publication No. US20030077646A1
: GENERAL INFORMATION:
: APPLICANT: GREG RISENECKER
: APPLICANT: SUMEDHA D. JAYASENA
: APPLICANT: LARRY GULD
: APPLICANT: DREW SMITH
: APPLICANT: GARY F. KIRSCHENHEIMER
: TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LEGAMUS HY
: SELEX
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESS: Swanson & Bratschus, S.L.C.
: STREET: 1745 Shea Center Drive, Suite 340
: CITY: Highlands Ranch
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80129
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
: COMPUTER: IBM pc compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WordPerfect 8.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/263,456
: FILING DATE: 02-Oct-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/606,477
: FILING DATE: 29-Jun-2000
: APPLICATION NUMBER: 08/956,699
: FILING DATE: OCTOBER 23, 1997
: APPLICATION NUMBER: 08/234,997
: FILING DATE: APRIL 28, 1994

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: APPLICATION NUMBER: 07/714,131
: FILING DATE: JUNE 10, 1991
: APPLICATION NUMBER: 07/536,428
: FILING DATE: JUNE 11, 1990
: APPLICATION NUMBER: 08/117,991
: FILING DATE: SEPTEMBER 6, 1994
: APPLICATION NUMBER: 08/123,935
: FILING DATE: SEPTEMBER 17, 1994
: APPLICATION NUMBER: 08/199,507
: FILING DATE: FEBRUARY 22, 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Barry J. Swanson
: REGISTRATION NUMBER: 33,215
: REFERENCE/DOCKET NUMBER: NEX15/C-CON
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 793-3333
: TELEFAX: (303) 793-3433
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-263-456-1

Query Match          100.0%; Score 35; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTTP 6
DB 1 GRGDTTP 6

RESULT 4
US-10-193-764-41
: Sequence 41, Application US/10193764
: Publication No. US20030133943A1
: GENERAL INFORMATION:
: APPLICANT: Loosmore, Sheena M.
: APPLICANT: Yang, Yan-Ping
: APPLICANT: Klein, Michel H.
: TITLE OF INVENTION: PROTECTIVE PEPTOMIMANT HAEMOPHILUS INFLUENZAE HIGH
: FILE REFERENCE: 1038-1239M1S
: CURRENT APPLICATION NUMBER: US/10/193,764
: CURRENT FILING DATE: 2002-07-12
: PRIOR APPLICATION NUMBER: 09/167,568
: PRIOR FILING DATE: 1998-10-07
: NUMBER OF SEQ ID NOS: 91
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 41
: LENGTH: 1005
: TYPE: PRT
: ORGANISM: Haemophilus influenzae
US-10-193-764-41

Query Match          100.0%; Score 35; DB 12; Length 1005;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTTP 6
DB 19 GRGDTTP 24

RESULT 5
US-10-193-764-39
: Sequence 39, Application US/10193764
: Publication No. US20030133943A1
: GENERAL INFORMATION:
: APPLICANT: Loosmore, Sheena M.

```

; APPLICANT: Yang, Yan-Ping  
 ; APPLICANT: Kleig, Michel B.  
 ; TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH  
 ; TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS  
 ; FILE REFERENCE: 1038-1239MIS  
 ; CURRENT APPLICATION NUMBER: US/10/193,764  
 ; PRIOR FILING DATE: 2002-07-12  
 ; PRIOR APPLICATION NUMBER: 09/167,566  
 ; PRIOR FILING DATE: 1998-10-07  
 ; NUMBER OF SEQ ID NOS: 91  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 39  
 ; TYPE: PRT  
 ; ORGANISM: Haemophilus influenzae  
 US-10-193-764-39

Query Match 100.0% Score 32; DB 12; Length 1517  
 Best Local Similarity 100.0%; Pred. No. 7.6e-02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6  
 111111  
 Db 25 GRGDTP 30

## RESULT 6

US-10-156-761-13265  
 ; Sequence 13265, Application US/0156761  
 ; Publication No. US20030119018A1

; GENERAL INFORMATION:  
 ; APPLICANT: OMURA, SATOSHI  
 ; APPLICANT: IKEDA, HARUO  
 ; APPLICANT: ISHIKAWA, JUN  
 ; APPLICANT: HORIKAWA, HIROSHI  
 ; APPLICANT: SHIDA, TADAYOSHI  
 ; APPLICANT: SAKAKI, YOSHIYUKI  
 ; APPLICANT: HATTORI, MASAHARA  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 ; FILE REFERENCE: 249-262  
 ; CURRENT APPLICATION NUMBER: US/10/156,761  
 ; CURRENT FILING DATE: 2002-05-29  
 ; PRIOR APPLICATION NUMBER: JP 2001-204089  
 ; PRIOR FILING DATE: 2001-05-30  
 ; PRIOR APPLICATION NUMBER: JP 2001-272597  
 ; PRIOR FILING DATE: 2001-09-02  
 ; NUMBER OF SEQ ID NOS: 15109  
 ; SEQ ID NO 13265  
 ; LENGTH: 1517  
 ; TYPE: PRT  
 ; ORGANISM: Streptomyces avermitilis

US-10-156-761-13265

Query Match 91.4% Score 32; DB 15; Length 1517;  
 Best Local Similarity 83.3%; Pred. No. 7.6e-02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6  
 111111  
 Db 1512 GRGDTP 1517

## RESULT 7

US-09-837-969A-28  
 ; Sequence 28, Application US/09837969A  
 ; Patent No. US20020030150A1

; GENERAL INFORMATION:  
 ; APPLICANT: Uryu, Dan  
 ; TITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration  
 ; FILE REFERENCE: BERL-020/030S  
 ; CURRENT APPLICATION NUMBER: US/09/837,969A  
 ; CURRENT FILING DATE: 2001-06-19  
 ; PRIOR APPLICATION NUMBER: US 09/258,723

; PRIOR FILING DATE: 1999-02-26  
 ; PRIOR APPLICATION NUMBER: US 60/087155  
 ; PRIOR FILING DATE: 1998-05-29  
 ; PRIOR APPLICATION NUMBER: US 60/076297  
 ; PRIOR FILING DATE: 1998-02-27  
 ; NUMBER OF SEQ ID NOS: 65  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 28  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)..(6)  
 ; OTHER INFORMATION: Synthetic  
 US-09-837-969A-28

Query Match 88.6% Score 31; DB 9; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 5e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6  
 111111  
 Db 1 GRGDSP 6

## RESULT 8

US-09-837-969A-46  
 ; Sequence 46, Application US/09837969A  
 ; Patent No. US20020038150A1

; GENERAL INFORMATION:  
 ; APPLICANT: Uryu, Dan  
 ; TITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration  
 ; FILE REFERENCE: BERL-020/030S  
 ; CURRENT APPLICATION NUMBER: US/09/837,969A  
 ; CURRENT FILING DATE: 2001-06-19  
 ; PRIOR APPLICATION NUMBER: US 09/258,723  
 ; PRIOR FILING DATE: 1999-02-26  
 ; PRIOR APPLICATION NUMBER: US 60/067155  
 ; PRIOR FILING DATE: 1998-05-29  
 ; PRIOR APPLICATION NUMBER: US 60/076297  
 ; PRIOR FILING DATE: 1998-02-27  
 ; NUMBER OF SEQ ID NOS: 65  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 46  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)..(6)  
 ; OTHER INFORMATION: Synthetic  
 US-09-837-969A-46

Query Match 88.6% Score 31; DB 9; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 5e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6  
 111111  
 Db 1 GRGDSP 6

## RESULT 9

US-09-888-260-15  
 ; Sequence 15, Application US/09888260  
 ; Patent No. US20020068304A1

; GENERAL INFORMATION:  
 ; APPLICANT: Bioelastics Research, Ltd.  
 ; APPLICANT: Uryu, Dan  
 ; TITLE OF INVENTION: Bioelastomer Nanomachines and Biosensors  
 ; FILE REFERENCE: BERL-030/010S  
 ; CURRENT APPLICATION NUMBER: US/09/888,260

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: CURRENT FILING DATE: 2001-06-21
: PRIOR APPLICATION NUMBER: 60/213,344
: PRIOR FILING DATE: 2003-06-23
: NUMBER OF SEQ ID NOS: 53
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 15
: LENGTH: 6
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: NAME/KEY: PETIDE
: LOCATION: (1)..(6)
: OTHER INFORMATION: Synthetic
US-09-888-260-15

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Query Match      88.6%; Score 31; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. Hits: 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GRGDTF 6
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Db      1 GRGDSP 6

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## RESULT 10

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US-09-961-834-1
: Sequence 1, Application US/09061834
: Patent No. US20020081726A;
: GENERAL INFORMATION:

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: APPLICANT: Russell et al.
: TITLE OF INVENTION: MICROFABRICATION OF MEMBRANES FOR THE GROWTH OF CELLS
: FILE REFERENCE: 27611/37761
: CURRENT APPLICATION NUMBER: US/09/961,834
: CURRENT FILING DATE: 2001-09-24
: PRIOR APPLICATION NUMBER: US 60/235,094
: PRIOR FILING DATE: 2000-09-25
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 6
: TYPE: PRT
: ORGANISM: Fibronectin ligand receptor
US-09-961-834-1

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```

Query Match      88.6%; Score 31; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. Hits: 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GRGDTF 6
      111111
Db      1 GRGDSP 6

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## RESULT 11

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US-09-364-597A-21
: Sequence 21, Application US/09364597A
: Patent No. US2002010330A1
: GENERAL INFORMATION:

```

```

: APPLICANT: Rosenthal, Erik
: APPLICANT: Koyuncu, Ekki
: TITLE OF INVENTION: No. US/09/364,597A; Integrated Binding Peptides
: NUMBER OF SEQUENCES: 46
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLC
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/364,597A
: FILING DATE: 30-JUL-1999
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/156,601
: FILING DATE: 24-NOV-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/285,861
: FILING DATE: 04-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-JA 3419
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (858) 535-9001
: TELEFAX: (858) 535-8949
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-09-364-597A-21

```

```

Query Match      88.6%; Score 31; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. Hits: 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GRGDTF 6
      111111
Db      1 GRGDSP 6

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## RESULT 12

```

US-09-177-843-1
: Sequence 1, Application US/09177843
: Patent No. US20020114804A1
: GENERAL INFORMATION:

```

```

: APPLICANT: THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE
: APPLICANT: CITY OF NEW YORK
: TITLE OF INVENTION: A METHOD OF PREVENTING AND TREATING
: TITLE OF INVENTION: BACTERIAL INFECTION OF SUTURES AND
: TITLE OF INVENTION: PROSTHETIC DEVICES, AND PROMOTING
: TITLE OF INVENTION: INGRESS OF LEUKOCYTES INTO TUMOR
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/177,843
: FILING DATE: April 22, 1997
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 48940-A-PCT/JPW/CKM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-278-0400
: TELEFAX: 212-391-0525
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids

```

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-177-843-1

Query Match 88.6%; Score 31; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. 5e-05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6  
| | | | |  
DB 1 GRGDSP 6

## RESULT 13

US-09-841-321A-28  
Sequence 28, Application US/09841321A  
Patent No. US20020116059A1  
GENERAL INFORMATION:  
APPLICANT: Urvy, Dan  
TITLE OF INVENTION: Injectable Implants for Tissue Augmentation and Restoration  
FILE REFERENCE: BERL-020/0405  
CURRENT APPLICATION NUMBER: US/09/841.321A  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: US 09/258.723  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: US 60/087155  
PRIOR FILING DATE: 1998-05-29  
PRIOR APPLICATION NUMBER: US 60/076297  
PRIOR FILING DATE: 1998-02-27  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 28  
LENGTH: 6  
TYPE: PRI  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(6)  
OTHER INFORMATION: Synthetic  
US-09-841-321A-28

Query Match 88.6%; Score 31; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. 5e-05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6  
| | | | |  
DB 1 GRGDSP 6

## RESULT 14

US-09-841-321A-46  
Sequence 46, Application US/09841321A  
Patent No. US20020116059A1  
GENERAL INFORMATION:  
APPLICANT: Urvy, Dan  
TITLE OF INVENTION: Injectable Implants for Tissue Augmentation and Restoration  
FILE REFERENCE: BERL-020/0405  
CURRENT APPLICATION NUMBER: US/09/841.321A  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: US 09/258.723  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: US 60/087155  
PRIOR FILING DATE: 1998-05-29  
PRIOR APPLICATION NUMBER: US 60/076297  
PRIOR FILING DATE: 1998-02-27  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 46

LENGTH: 6  
TYPE: PRI  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(6)  
OTHER INFORMATION: Synthetic  
US-09-841-321A-46

Query Match 88.6%; Score 31; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. 5e-05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6  
| | | | |  
DB 1 GRGDSP 6

## RESULT 15

US-09-871-974-3  
Sequence 3, Application US/09871974  
Patent No. US20020147136A1  
GENERAL INFORMATION:  
APPLICANT: VON WRONSKI, MATHEW A.  
APPLICANT: MARINELLI, EDMUND R.  
APPLICANT: NUNN, ADRIAN D.  
APPLICANT: PILLAI, RADHAKRISHNA  
APPLICANT: RAMALINGAM, KONDAREDDI, AR  
APPLICANT: TWEDDE, MICHAEL F.  
APPLICANT: LINDER, KAREN  
APPLICANT: NANJAPPAN, PALANIAPPA  
APPLICANT: RAJU, NATARAJAN  
TITLE OF INVENTION: COMPOUNDS FOR TARGETING ENDOHELIAL CELLS, COMPOSITIONS  
FILE REFERENCE: 2238-7  
CURRENT APPLICATION NUMBER: US/09/871.974  
CURRENT FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 09/585.364  
PRIOR FILING DATE: 2000-06-02  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 6  
TYPE: PRI  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
US-09-871-974-3

Query Match 88.6%; Score 31; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. 5e-05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6  
| | | | |  
DB 1 GRGDSP 6

Search completed: September 16, 2003, 15:18:56  
Job time : 27 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2003, 14:15:07 / Search time 15 Seconds  
(without alignments)  
34,462 Million cell updates/sec

Title: US-09-780-612A-1

Perfect score: 35

Sequence: 1 GRGDIP 6

Scoring table: HUSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616662 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 3

Maximum DB seq length: 2500000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR\_761

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	370	2 S27344	luck protein - Rhi
2	35	100.0	450	2 D87342	multidrug resist
3	35	100.0	1307	2 T30867	246D nuclear prote
4	32	91.4	266	1 S8159	ribosomal protein
5	32	91.4	458	2 T32571	probable myosinas
6	32	91.4	606	2 AC2508	hypothetical prote
7	32	91.4	1226	2 S44824	F54F2.2 protein -
8	31	88.6	273	2 A28512	fibronectin - chi
9	31	88.6	359	2 S84270	hypothetical prote
10	31	88.6	425	1 S88469	probable membrane
11	31	88.6	438	2 B82042	osmolarity sensor
12	31	88.6	441	2 S74264	isocitrate synt
13	31	88.6	463	1 S74845	tidb homolog sir08
14	31	88.6	515	2 A39675	probable oxidoredu
15	31	88.6	515	2 D95525	probable oxidoredu
16	31	88.6	606	2 T33100	hypothetical prote
17	31	88.6	691	2 T45333	hypothetical prote
18	31	88.6	1020	2 A29385	fibronectin - chi
19	31	88.6	2265	1 FN80	fibronectin - chi
20	31	88.6	2386	1 FN80	fibronectin precu
21	31	88.6	2477	2 S14424	fibronectin precu
22	31	88.6	2481	2 A43928	fibronectin - ARI
23	30	85.7	253	2 S84258	hypothetical prote
24	30	85.7	277	2 A33256	aminoglycoside (EC
25	30	85.7	299	2 C55213	rbc protein - Shi
26	30	85.7	317	2 A75477	cysteine synthase
27	30	85.7	335	1 KPR08	cathepsin B (EC 3.
28	30	85.7	339	1 KHR08	cathepsin B (EC 3.
29	30	85.7	339	1 KHR08	cathepsin B (EC 3.

ALIGNMENTS

RESPT 1  
S27344  
hupx protein - Rhizobium leguminosarum  
C:Species: Rhizobium leguminosarum  
C:Date: 25-Oct-1994 #sequence\_revision 01-Dat-1995 #text\_change 08-Oct-1999  
C:Accession: S27344  
R:Ref: L. Hidalgo, E. Palacios, J. Ruiz-Arguieso, E.  
C. Mol. Biol. 226, 998-1002, 1992  
A:Title: Nucleotide sequence and organization of an hupX(2) uptake gene cluster from Rhi  
A:Reference number: S27340; X010:93108466; PMID:1459753  
A:Accession: S27344  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-370 <RAY>  
A:Cross-references: EMBL:X52974; NID:q167855; PIRN:CAA97156.1; PIR:q48731  
Query Match 100.0% Score 35; DB 2; Length 370;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDIP 6  
DB 163 GRGDIP 168

RESULT 2  
D87342  
multidrug resistance protein, probable (imported) - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001  
C:Accession: D87342  
K:Neuman, W.C.; Feldblyum, T.V.; Paulsen, I.I.; Nelson, K.E.; Eisen, J.; Heidelberg,  
B.; Laub, M.T.; Deboy, K.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.L.; K  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, J.; Venter, J.C.; Fraser, J  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; X010:21173698; PMID:11259667  
A:Accession: D87342  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-450 <STO>  
A:Cross-references: GB:AE005673; NID:g13421986; PIRN:AAK22736.1; GSPDB:GN00148  
C:Genetics:  
A:Gene: CC0751

Query Match 100.0% Score 35; DB 2; Length 450;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDIP 6  
DB 220 GRGDIP 225

C:Accession: T02571; G84815  
 R:Kounisloy, S.D.; Kaul, S.; Liu, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke  
 submitted to the EMBL Data Library, August 1998  
 A:Description: Arabidopsis thaliana chromosome II PAC T16B24 genomic sequence.  
 A:Reference number: 214619  
 C:Accession: T02571  
 A:Status: Translated from GS/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-458 <R00>  
 A:Cross-references: EMBL:AC004597; NID:q3402671; FID:q3402671  
 A:Experimental source: Cultivar Columbia  
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shree, J.P.; Ruito, M.L.; Town, C.D.; Fujii, C.Y.  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VarAken, S.E.; Umayam, L.; Telson,  
 Gess, D.; Nicmar, W.C.; White, G.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  
 Nature 402, 761-768, 1999  
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; MUID:20083487; PMID:10617197  
 A:Accession: G84815  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-458 <STO>  
 A:Cross-references: GB:AE002693; NID:q3402676; PID:AC023979.1; GSPDB:GN00139  
 C:Genetics:  
 A:Gene: T16B24.5; At2g39310  
 A:Map position: 2  
 A:Introns: 67/3; 221/3; 374/3  
 Query Match 91.4%; Score 32; DB 2; Length 458;  
 Best Local Similarity 83.3%; Pred. No. 97;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGDTP 6  
 Db 214 GRGDTP 219  
 I:|||||  
 RESULT 6  
 AC2508  
 hypothetical protein alr7243 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC712  
 C:Species: Nostoc sp. PCC 7120  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
 C:Accession: AC2508  
 R:Kakazu, T.; Nakamura, Y.; Wolk, C.P.; Kurita, T.; Susamoto, S.; Watanabe, A.; Iriku  
 Kakazu, N.; Shimpou, S.; Sugimoto, Y.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium  
 A:Reference number: AB1807; MUID:21595235; PMID:11759840  
 A:Accession: AC2508  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-606 <KUR>  
 A:Cross-references: GB:BA000320; PID:BA000320.1; PID:q17195781; GSPDB:GN00180  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: alr7243  
 A:Genome: plasmid  
 Query Match 91.4%; Score 32; DB 2; Length 606;  
 Best Local Similarity 83.3%; Pred. No. 76;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGDTP 6  
 Db 120 GRGDTP 125  
 I:|||||  
 RESULT 7  
 S44824  
 154f2.1 protein - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 A:Title: 154f2.1 protein (mouse-ear cress)  
 C:Date: 14-Sep-1994 #sequence\_revision 12-May-1995 #text\_change 23-Mar-2001  
 C:Accession: S44824

RESULT 3  
 T30887  
 146D nuclear protein - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 20-Jul-2000  
 C:Accession: T30887  
 R:Schmidt-Zachmann, M.S.; Knecht, S.; Kraemer, A.  
 Mol. Biol. Cell 9, 143-160, 1998  
 A:Title: Molecular characterization of a novel, widespread nuclear protein that colocal  
 A:Reference number: 220921; MUID:94092693; PMID:9445997  
 A:Accession: T30887  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1307 <SCH>  
 A:Cross-references: EMBL:Y08997; NID:q2791835; PID:CAA70201.1; PID:q2791896

Query Match 100.0%; Score 35; DB 2; Length 1307;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGDTP 6  
 Db 272 GRGDTP 277  
 I:|||||

RESULT 4  
 S18159  
 ribosomal protein L7a, cytosolic - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 22-Jun-1999  
 R:Colombo, P.; Yon, J.; Garson, K.; Fried, M.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 6358-6362, 1993  
 A:Title: Conservation of the organization of five tightly clustered genes over 600 mill  
 A:Reference number: A46032; MUID:92335297; PMID:1631131  
 A:Accession: A46032  
 A:Molecule type: mRNA; DNA  
 A:Residues: 1-266 <COL>  
 A:Cross-references: EMBL:X62640; NID:q63777; PID:CAA44505.1; PID:q63778  
 A:Note: submitted to the EMBL Data Library, October 1991  
 A:Note: sequence extracted from NCBI backbone (NCBI:P:108713)  
 R:Maeda, N.; Kenmochi, N.; Tanaka, T.  
 Biochimie 75, 785-790, 1993  
 A:Title: The complete nucleotide sequence of chicken ribosomal protein L7a gene and the  
 A:Reference number: 150416; MUID:94160270; PMID:8274596  
 A:Accession: 150416  
 A:Status: Translated from GS/EMBL/DBJ  
 A:Molecule type: rRNA  
 A:Residues: 1-266 <MAE>  
 A:Cross-references: GB:U14522; NID:q457652; PID:BA00095.1; PID:q457654  
 C:Genetics:  
 A:Gene: surr-3/Rp.7a  
 A:Introns: 1/3; 42/1; 92/1; 139/1; 165/3; 259/2; 232/3  
 C:Superfamily: rat ribosomal protein L7a  
 C:Keywords: protein biosynthesis; ribosome

Query Match 91.4%; Score 32; DB 1; Length 266;  
 Best Local Similarity 83.3%; Pred. No. 32;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGDTP 6  
 Db 124 GRGDTP 129  
 I:|||||

RESULT 5  
 T02571  
 probable myosinase-binding protein [imported] - Arabidopsis thaliana  
 A:Alternate names: hypothetical protein T16B24.5  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 16-Feb-2001



R:Anderson, K.  
submitted to the EMBL Data Library, September 1993  
A:Description: Sequence of the *C. elegans* cosmid F54F2.  
A:Reference number: S44827  
A:Accession: S44824  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1226 <AND>  
A:Cross-references: EMBL:L23645; NID:q388603; PID:q388605  
C:Genetics:  
A:Introns: 58/2; 137/3; 179/2; 316/2; 393/1; 552/3; 597/2; 652/2; 855/3; 1178/1  
C:Keywords: cytoskeleton; transmembrane protein

Query Match 81.4%; Score 31; DB 2; Length 1226;  
Best Local Similarity 83.3%; Pred. No. 53;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6  
IIIIII

DB 519 GRGDTP 524

RESULT 8  
A28512  
fibronectin - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 31-Dec-1988 #sequence\_revision 1; text\_change 20-Aug-1993  
C:Accession: A28512  
R:Kubomura, S.; Goara, M.; Kanasaka, Y.; Tadokuchi, H.; Gotoh, S.; Tsuka, T.; Hiroshi, K.  
Biochim. Biophys. Acta 910, 171-181, 1987  
A:Title: Genetic analysis of the cell binding domain region of the chicken fibronectin  
A:Reference number: A28512; MIM:282389; PMID:282389  
A:Accession: A28512  
A:Molecule type: DNA  
A:Residues: 1-273 <KOR>  
A:Cross-references: GB:X06533; NID:q36393; PID:CAA29761.1; PID:q297716  
A:Note: The authors translated the codon CCG for residue 190 as Gln, CAG for residue 243  
C:Genetics:  
A:Introns: 90/1; 123/1; 184/1; 236/1  
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat  
C:Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heter  
F:1-82/Domain: fibronectin type III repeat homology (fragment) <FNIII>  
F:90-172/Domain: fibronectin type III repeat homology <FN3D>  
F:167-169/Region: cell attachment (R-G-D) motif  
F:184-266/Domain: fibronectin type III repeat homology <FN3K>

Query Match 89.6%; Score 31; DB 2; Length 273;  
Best Local Similarity 83.3%; Pred. No. 53;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6  
IIIIII

DB 166 GRGDSP 171

RESULT 9  
G84270  
hypothetical protein Vng1149c [imported] - Halobacterium sp. NRC-1  
C:Species: Halobacterium sp. NRC-1  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: G84270  
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Patz, M.; Shukla, H.; Lasky, S.  
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, J.D.; Jablo  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Greer, A.D.; Elhardt, H.; Lowe, T.M.; Li  
A:Title: Genome sequence of Halobacterium species NRC-1.  
A:Reference number: A84160; MIM:2050446; PMID:11016950  
A:Accession: G84270  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-399 <STO>  
A:Cross-references: GB:AE004437; NID:gl0580687; PID:AAGL1531.1; GSPB:GN04138

C:Genetics:  
A:Gene: VNG1149C

Query Match 88.6%; Score 31; DB 2; Length 399;  
Best Local Similarity 83.3%; Pred. No. 89;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6  
IIIIII

DB 287 GRGETP 292

RESULT 10  
S48459  
probable membrane protein YII133w - yeast (Saccharomyces cerevisiae)  
C:Species: Saccharomyces cerevisiae  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 19-Apr-2002  
C:Accession: S48459  
R:Howman, S.; Churcher, C.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S48455  
A:Accession: S48459  
A:Molecule type: DNA  
A:Residues: 1-425 <BOV>  
A:Cross-references: GB:Z47047; EMBL:Z4825; NID:q763243; GSPB:GN03009;  
C:Genetics:  
A:Gene: MIPSA:YII133w  
A:Cross-references: SGD:SC000135  
A:Map position: 9L  
C:Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1803  
C:Keywords: transmembrane protein  
F:155-177/Domain: transmembrane #status predicted <TM>  
F:334-350/Domain: transmembrane #status predicted <TM2>

Query Match 86.6%; Score 31; DB 1; Length 425;  
Best Local Similarity 83.3%; Pred. No. 85;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6  
IIIIII

DB 415 GRGETP 420

RESULT 11  
S82042  
osmolarity sensor protein EnvZ VC2713 [imported] - Vibrio cholerae (strain N1695; se  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C:Accession: S82042  
R:Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Swinn, M.L.; Dodson, R.  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Saller,  
L. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
A:Reference number: A82035; MIM:2046833; PMID:10952401  
A:Accession: S82042  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-438 <HKL>  
A:Cross-references: GB:AE004337; GB:AE003852; NID:q9457307; PID:AAFP95853.1; GSPB:G  
A:Experimental source: serogroup O1; strain N1695; biotype E1 Tor  
C:Genetics:  
A:Gene: VC2713  
A:Map position: 1

Query Match 88.6%; Score 31; DB 2; Length 438;  
Best Local Similarity 83.3%; Pred. No. 88;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6  
IIIIII

DB 190 GRGETP 195

```

RESULT 12
E84264
isochorismate synthase [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: E84264
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.B.; Periquist, H.; Fan, M.; Soule, H.D.; Dasky, S.;
Leithauser, B.; Keller, K.; Cruz, R.; Dawson, M.J.; Hord, D.W.; Madhock, D.O.; Jahn,
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hord, S.; Dancels, C.J.; Dennis, P.F.; Oert, A.D.; Bhattach, H.; Lowe, T.M.; Le
A:Title: Genome sequence of Halobacterium species NRC-1
A:Reference number: A84160; MUID:20504483; PMID:11131692
A:Accession: E84264
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-441 <STO>
A:Cross-references: GB:AE004437; NID:91058029; PIRN:AA019411; GSPDB:GN00138
C:Genetics:
A:Gene: menF

Query Match 86.6%; Score 31; DB 2; Length 441;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6
|||||
DB 271 GRGDSP 276

RESULT 13
S74845
tldD homolog slr0863 - Synecocystis sp. (strain PCC 6603)
C:Species: Synecocystis sp.
A:Variety: PCC 6603
C:Date: 29-Jan-1999 #sequence_revision 29-Jan-1999 #text_change 16-Jun-2006
C:Accession: S74845
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watarabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
S.
A:Reference number: S74322; MUID:97051201; PMID:8905291
A:Accession: S74845
A:Molecule type: DNA
A:Residues: 1-463 <KAN>
A:Cross-references: EMBL:090909; GB:AH001349; NID:01652844; PIRN:KAA12906; E: EMBL:01652848
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: Escherichia coli tldC protein

Query Match 88.6%; Score 31; DB 1; Length 463;
Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6
|||||
DB 352 GRGETP 357

RESULT 14
A99675
probable oxidoreductase subunit ynfH [imported] - Escherichia coli (strain O157:H7, s
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: A99675
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Imai, C.O.;
gasawara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A99675
A:Status: preliminary

```

```

A:Molecule type: DNA
A:Residues: 1-515 <HAY>
A:Cross-references: GB:BA000007; PIRN:BA033792; E: EMBL:01658926; GSPDB:GN00154
A:Experimental source: strain O157:H7, Substrain KMD 050992
C:Genetics:
A:Gene: EEC0369

Query Match 88.6%; Score 31; DB 2; Length 515;
Best Local Similarity 83.3%; Pred. No. 16+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6
|||||
DB 284 GRGETP 289

RESULT 15
B85525
probable oxidoreductase subunit ynfH [imported] - Escherichia coli (strain O157:H7, s
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: D85525
R:Perica, N.T.; Plunkett III, G.; Burland, V.; Mau, H.; Glasner, J.D.; Rose, D.J.; May
ilicz, L.; Grobeck, E.J.; Davis, N.W.; Film, A.; Damalanta, E.; Potamoudis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074535; PMID:11206551
A:Accession: D85525
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-515 <STO>
A:Cross-references: GB:AE005174; NID:91253137; PIRN:AA054664; E: GSPDB:GN00145; JMWGP:
A:Experimental source: strain O157:H7, Substrain EDL933
C:Genetics:
A:Gene: ynfH

Query Match 88.6%; Score 31; DB 2; Length 515;
Best Local Similarity 83.3%; Pred. No. 16+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6
|||||
DB 284 GRGETP 289

Search completed: September 16, 2003, 18:14:01
Job time : 16 secs

```

GenCorp version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 16, 2003, 19:13:27 : Search time 12 seconds  
(without alignments)  
23,523 Million cell updates/sec

Title: US-09-780-612A-1

Perfect score: 35

Sequence: 1 GSGTTP 5

Scoring table: BLOSUM62

Gapop 12.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 6

Maximum DB seq length: 260000000

Post-processing: Minimum Match 04

Maximum Match 2004

Listing first 45 summaries

Database : SwissProt\_41\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being listed and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Description	ID
1	35	100.0	P29153 rhizobium l	HUPK_RHILV
2	35	100.0	O75533 homo sapien	S381_HUMAN
3	35	100.0	O99689 mus musculu	S381_MOUSE
4	35	100.0	O57683 xenopus lae	S381_XENLA
5	32	91.4	P34229 galus gall	R17A_CHICK
6	32	91.4	O80950 arabidopsis	MB22_ARATH
7	32	91.4	P34446 caecoriadi	PAT2_CAEEL
8	31	88.6	P46487 saccharomyc	YIK3_YEAST
9	31	88.6	P73754 synerdocyst	Y863_SYNY3
10	31	88.6	P11722 galus gall	FINC_CHICK
11	31	88.6	O91269 p.auridules	FINC_FLEWA
12	31	88.6	P07559 bos taurus	FINC_BOVIN
13	31	88.6	P02751 homo sapien	FINC_HUMAN
14	31	88.6	P11276 mus musculu	FINC_MOUSE
15	31	88.6	P04937 rattus norv	FINC_RAT
16	31	88.6	O91240 xenopus lae	FINC_XENLA
17	30	85.7	O99459 halobacteri	G332_HALNI
18	30	85.7	P37788 shigella fi	RFB1_SHIFL
19	30	85.7	P07698 bos taurus	CATR_BOVIN
20	30	85.7	P07558 homo sapien	CATR_HUMAN
21	30	85.7	P10605 mus musculu	CATR_MOUSE
22	30	85.7	P03787 rattus norv	CATR_RAT
23	30	85.7	P04757 rattus norv	ACR3_RAT
24	30	85.7	O5X808 streptomyces	NAB2_STRCO
25	30	85.7	P26791 daucus caro	H570_DAUCA
26	30	85.7	O452e6 homo sapien	SM6A_HUMAN
27	29	82.9	O98004 mycobacteri	R159_MYCLE
28	29	82.9	P38136 escherichia	KSEA_ECOLI
29	29	82.9	O54117 rhodococcus	NHAB_RHOSO
30	29	82.9	P17055 rhodobacter	CRTA_RHOCB
31	29	82.9	P21771 saccharomyc	R128_YEAST
32	29	82.9	P03359 simian sarc	POL_SMSAV
33	29	82.9	P27745 alcaligenes	ACCA_ALCEU

34	29	82.9	343	1	GAS1_MOUSE	Q01721 mus musculu
35	29	82.9	345	1	GAS1_HUMAN	P54826 homo sapien
36	29	82.9	367	1	RECF_CAUCK	P49998 caulobacter
37	29	82.9	425	1	POH1_BRARE	P31366 brachydanio
38	29	82.9	432	1	LMB1_VIBPA	P59494 vibrio para
39	29	82.9	436	1	IBX6_HUMAN	O95947 homo sapien
40	29	82.9	443	1	2P23_BRARE	P79745 brachydanio
41	29	82.9	467	1	VE2_HPV24	P50770 human papil
42	29	82.9	493	1	CPE1_HUMAN	P05181 homo sapien
43	29	82.9	493	1	CPE1_MESAU	P51561 mesocricetu
44	29	82.9	493	1	CPE1_MOUSE	Q05421 mus musculu
45	29	82.9	493	1	CPE1_RAT	P05182 rattus norv

## ALIGNMENTS

### RESULT 1

HUPK\_RHILV STANDARD: FRG: 370 AA.  
AC P29153:  
QT 01-JUL-1993 (Rel. 26, Created)  
QT 01-FEB-1996 (Rel. 33, Last sequence update)  
ET 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Hydrogenase expression/formation protein hupK.  
GN HUPK.  
OS Rhizobium leguminosarum (biovat viciae).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium/Azorhizobium group; Rhizobium  
OX NCBI\_TaxID:387;  
RN [1]  
RS SEQUENCE FROM N.A.  
RC STRAIN J28C53;  
BX MEDLINE:93108466; PubMed:1469733;  
RA Roy J., Hidalgo E., Palacios J.M., Ruiz-Argueso T.;  
RT "Nucleotide sequence and organization of an hz uptake gene cluster  
from Rhizobium leguminosarum bv. viciae containing a rhizodioxin-like  
gene and four additional open reading frames.";  
RC J. Mol. Biol. 228:998-1002(1992).  
BK [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:95020662; PubMed:7934943;  
RA Imperial J., Roy L., Ruiz-Argueso T.;  
RT "HupK, a hydrogenase-ancillary protein from Rhizobium leguminosarum,  
shares structural motifs with the large subunit of Nite hydrogenases  
and could be a scaffolding protein for hydrogenase metal cofactor  
assembly.";  
RT assembly.";  
RN Mol. Microbiol. 9:1305-1306(1993).  
BK [3]  
RS SEQUENCE FROM N.A.  
RC STRAIN-B10;  
RA Rito B., Palacios J.M., Imperial J., Ruiz-Argueso T., Yang W.C.,  
Bissegger T., Schmitt H., Keri V., Bauer T., Kokorek W., Lotz W.;  
RT "Organization of the hup-region and its differential transcription  
in non-symbiotic and symbiotic cells of Rhizobium leguminosarum  
bv. viciae B10.";  
RC Mol. Plant Microbe Interact. 8:235-240(1997).  
BK [4]  
RS SIMILARITY: BELONGS TO THE HUPK FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: X52974; CAA37158.1;  
CC EMBL: Z36981; CAA85440.1;  
CC PIR: S27344; S27344.  
CC CONF-LCT 240 240 A -> R (IN REF. 1).  
CC SEQUENCE 370 AA; 38751 MW; ED17BC76B52F26C9 CRO64;

Query Match 100.0%; Score 35; DB 1; Length 370;  
 Best Local Similarity 100.0%; Pred. No. 3.2;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 GRGDTP 6  
 DB 163 GRGDTP 168

RESULT 2  
 S3B1\_HUMAN STANDARD; PRT: 1304 AA.  
 ID S3B1\_HUMAN  
 AC Q75533;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DI 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Splicing factor 3B subunit 1 (Spliceosome associated protein 155) (SAP 155) (SF3B155) (Pre-mRNA splicing factor SF3B 155 kDa subunit).  
 GN SF3B1 OR SAPI55.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION.  
 RX MEDLINE=98252826; PubMed=9585501;  
 RA Wang C., Chua K., Sequenzi W., Lees E., Gozani O., Reed R.J.  
 RT "Phosphorylation of spliceosomal protein SAP 155 coupled with splicing catalysis.";  
 RL Genes Dev. 12:1409-1414(1998).  
 RN [2]  
 RP SEQUENCE OF 1011-1304 FROM N.A.  
 RC TISSUE=Brain;  
 RA Yu W., Gibbs R.A.;  
 RN [3]  
 RP Submitted (JUN-1998) to the EMBL/GenBank/CCBJ databases.  
 RN [3]  
 RP CHARACTERIZATION OF THE SPLICesome.  
 RX MEDLINE=20337962; PubMed=10862114;  
 RA Das R., Zhou Z., Reed R.J.  
 RT "Functional association of U2 snRNP with the ATP-independent spliceosomal complex E.";  
 RL Mol. Cell 5:779-787(2000).  
 CC -!- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3B REQUIRED FOR 'A' COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE BRANCHPOINT SEQUENCE (HPS) IN PRE-MRNA. SEQUENCE INDEPENDENT BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS ESSENTIAL. IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX. BELONGS ALSO TO THE MINOR U12-DEPENDENT SPLICesome, WHICH IS INVOLVED IN THE SPLICING OF RARE CLASS OF NUCLEAR PRE-MRNA INTRON (BY SIMILARITY).  
 CC -!- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3B WHICH IS COMPOSED OF FOUR SUBUNITS: SF3B4/SAP49, SF3B3/SAP130, SF3B2/SAP145, AND A SF3B1/SAPI55. SF3B ASSOCIATES WITH THE SPLICING FACTOR SF3A AND A 12S RNA UNIT TO FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP). SF3B1 INTERACTS DIRECTLY WITH THE SPLICING FACTOR U2AF.  
 CC -!- SUBCELLULAR LOCATION: NUCLEAR SPECKLES. DURING MITOSIS, TRANSIENTLY DISPERSED FROM THE NUCLEAR SPECKLES TO THE CYTOSOL.  
 CC -!- PTM: PHOSPHORYLATED. PHOSPHORYLATION OCCURS CONCOMITANT WITH THE CATALYTIC STEPS OF SPLICING.  
 CC -!- SIMILARITY: BELONGS TO THE SF3B1 FAMILY.  
 CC -!- SIMILARITY: Contains 2 HEAT repeats.

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 CC -----  
 CC EMBL; AF054284; AAC97189.1;  
 CC EMBL; AF070540; AAC28633.1;  
 CC -----  
 CC DR AF054284; AAC97189.1;  
 CC DR EMBL; AF070540; AAC28633.1;  
 CC KW Spliceosome: mRNA processing; mRNA splicing; Nuclear protein.

DR Genes: HGNC:10768; SF3B1.  
 DR CK: Q75533;  
 DR MM: 605590;  
 DR CC: GO:0005681; C:spliceosome complex; NAS.  
 DR GO: 00:0008248; P:pre-mRNA splicing factor activity; NAS.  
 DR GO: 00:0006371; P:mRNA splicing; NAS.  
 DR GO: 00:0006371; P:mRNA splicing; NAS.  
 KW Spliceosome: mRNA processing; mRNA splicing; Nuclear protein;  
 KW phosphorylation; Repeat.  
 SO SEQUENCE 1304 AA; 145814 MB; 40821A62691E9A7 CDS64;

Query Match 100.0%; Score 35; DB 1; Length 370;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 GRGDTP 6  
 DB 269 GRGDTP 274

RESULT 3  
 S3B1\_MOUSE STANDARD; PRT: 1304 AA.  
 ID S3B1\_MOUSE  
 AC Q99NB9;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DI 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Splicing factor 3B subunit 1 (Spliceosome associated protein 155) (SAP 155) (SF3B155) (Pre-mRNA splicing factor SF3B 155 kDa subunit).  
 GN SF3B1 OR SAPI55.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Scleroglossa; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=21189985; PubMed=11252167;  
 RA Isomura K., Abe K., Tomari Y., Kikuchi Y., Hayashizaki Y., Koseki H.;  
 RT "Molecular cloning, genetic mapping, and expression of the mouse Sf3b1 (SAP155) gene for the U2snRNP component of spliceosome.";  
 RL Mamm. Genome 12:192-198(2001).  
 CC -!- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3B REQUIRED FOR 'A' COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE BRANCHPOINT SEQUENCE (HPS) IN PRE-MRNA. SEQUENCE INDEPENDENT BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS ESSENTIAL. IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX. BELONGS ALSO TO THE MINOR U12-DEPENDENT SPLICesome, WHICH IS INVOLVED IN THE SPLICING OF RARE CLASS OF NUCLEAR PRE-MRNA INTRON (BY SIMILARITY).  
 CC -!- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3B WHICH IS COMPOSED OF FOUR SUBUNITS: SF3B4/SAP49, SF3B3/SAP130, SF3B2/SAP145, AND A SF3B1/SAPI55. SF3B ASSOCIATES WITH THE SPLICING FACTOR SF3A AND A 12S RNA UNIT TO FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP). SF3B1 INTERACTS DIRECTLY WITH THE SPLICING FACTOR U2AF.  
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (By similarity).  
 CC -!- TISSUE SPECIFICITY: Ubiquitous.  
 CC -!- PTM: PHOSPHORYLATED. PHOSPHORYLATION OCCURS CONCOMITANT WITH THE CATALYTIC STEPS OF SPLICING (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE SF3B1 FAMILY.  
 CC -!- SIMILARITY: Contains 2 HEAT repeats.

-----  
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 CC -----  
 CC EMBL; AB037890; BAB40140.1;  
 CC EMBL; MGI:1932339; Sf3b1.  
 CC -----  
 CC DR MGI:1932339; Sf3b1.  
 CC KW Spliceosome: mRNA processing; mRNA splicing; Nuclear protein.

KW Phosphorylation; Repeat.  
SQ SEQUENCE 1304 AA: 145816 MW: 12905175702A2DEE CRC64:

Query Match 100.0%; Score 35; DB 1; Length 1304;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6  
|||||  
DB 269 GRGDP 274

RESULT 4  
S3BL\_XENIA STANDARD: PRT: 1307 AA.

ID S3BL\_XENIA  
AC 057633;  
DT 16-OCT-2001 (Rel. 40, Created)  
DI 16-OCT-2001 (Rel. 40, Last sequence update)  
DE Splicing factor 3b subunit 1 (Spliceosome associated protein 155) (SAP155) (S3BL155) (Pre-mRNA splicing factor SF3B155 kDa subunit) [14]  
DE kDa nuclear protein).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID:8355;  
RN 1;  
RP SEQUENCE FROM N.A.  
RX MEDLINE:98095935; PubMed:9446947;  
RA Schmidt-Zachmann M.S., Kroetz S., Kraemer A.  
RT "Molecular characterization of a novel, widespread nuclear protein  
RL Mol. Biol. Cell. 9:143-160(1998).  
CC -!- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3B REQUIRED FOR THE  
CC COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE  
CC BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT  
CC BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS  
CC ESSENTIAL. IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE  
CC INVOLVED IN THE ASSEMBLY OF THE 70S COMPLEX. BELONGS ALSO TO THE  
CC MINOR U12-DEPENDENT SPLICOSOME, WHICH IS INVOLVED IN THE SPLICING  
CC OF RARE CLASS OF NUCLEAR PRE-MRNA INTRON (BY SIMILARITY).  
CC -!- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3B WHICH IS COMPRISED OF  
CC FOUR SUBUNITS: SF3H4/SAP19, SF3H1/SAP130, SF352/SAP145,  
CC SF3B1/SAP155. SF3B ASSOCIATES WITH THE SPLICING FACTOR SF3A AND A  
CC 12S RNA UNIT TO FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEINS  
CC COMPLEX (U2 SNRNP) (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- SIMILARITY: BELONGS TO THE SF3B1 FAMILY.  
CC -!- SIMILARITY: Contains ? HEAT REPEATS.

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EMBL: Y08897; CAA70201.1;  
DR PIR: T30887; T30887.  
KW Spliceosome; mRNA processing; mRNA splicing; Nuclear protein;  
KW Repeat.  
SQ SEQUENCE 1307 AA: 146213 MW: 632260503606953 CRC64:

Query Match 100.0%; Score 35; DB 1; Length 1307;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6  
|||||  
DB 272 GRGDP 277

RESULT 5  
KL7A\_CHICK STANDARD: PRT: 265 AA.

ID KL7A\_CHICK  
AC P32429;  
DT 01-OCT-1993 (Rel. 27, Created)  
DI 01-OCT-1993 (Rel. 27, Last sequence update)  
DI 01-FEB-1996 (Rel. 33, Last annotation update)  
DE 50S ribosomal protein L7a.  
DE KL7A OR SURF-3.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID:9031;  
RN 1;  
RP SEQUENCE FROM N.A.  
RX TISSUE=Liver;  
RX TISSUE=Liver;  
RX MEDLINE:92335297; PubMed:1631131;  
RA Colombo P., Yon J., Garson K., Fried M.  
RT "Conservation of the organization of five tightly clustered genes  
RE over 600 million years of divergent evolution".  
RC Proc. Natl. Acad. Sci. U.S.A. 89:6358-6362(1992).  
RN 12;  
RP SEQUENCE FROM N.A.  
RX TISSUE=Liver;  
RX TISSUE=Liver;  
RX MEDLINE:94100270; PubMed:8274530;  
RA Maeda N., Kenmochi N., Tanaka T.  
RT "The complete nucleotide sequence of chicken ribosomal protein L7a  
RE gene and the multiple factor binding sites in its 5' flanking  
RC region".  
RC Biochimie 75:785-790(1993).  
CC -!- SIMILARITY: BELONGS TO THE L7AE FAMILY OF RIBOSOMAL PROTEINS.

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EMBL: X62640; CAA44506.1;  
DR EMBL: D14522; BAA03395.1;  
DR PIR: A46032; S19159.  
DR InterPro: IPR004038; Ribosomal\_L7A.  
DR Pfam: PF01248; Ribosomal\_L7Ae; 1.  
DR PRINTS: PR00881; L7ARS6PAMILY.  
DR PROSITE: PS01082; RIBOSOMAL\_L7AE; 1.  
KW Ribosomal protein.  
FT INIT\_MET 0  
SQ SEQUENCE 265 AA: 29868 MW: 07E312G639B5655 CRC64:

Query Match 91.4%; Score 32; DB 1; Length 265;  
Best Local Similarity 83.3%; Pred. No. 10;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6  
|||||  
DB 123 GRGDP 128

RESULT 6  
MF22\_ARATH STANDARD: PRT: 458 AA.

ID MF22\_ARATH  
AC O80950;  
DI 16-OCT-2001 (Rel. 40, Created)  
DI 16-OCT-2001 (Rel. 40, Last sequence update)  
DI 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Myosinase binding protein-like Atg39310.  
DE ATG39310 OR T16B24.5.  
OS Arabidopsis thaliana (Mouse-ear cress).

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Eucaryotophyta;  
 CC Spermatophyta; Magnoliophyta; Eudicotyledons; Ericales; Rosales;  
 CC Eucotyledons II; Brassicales; Brassicaceae; Arabidopsis  
 CC NCBI\_TaxID=1072;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=cv. Columbia  
 CC MEDLINE=20061487; PubMed=16617197;  
 CC Lin X., Kaul S., Kounsley S.D., Shea J.P., Beilke M., Lee T.W., Chao  
 CC Fujii C.Y., Mason T.M., Rasmussen C.L., Rasmussen M.E., Rasmussen T.W.,  
 CC Buell C.R., Ketchum K.A., Lee J.C., Rasmussen C.L., Koo H.L.,  
 CC Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Mayday L.,  
 CC Tallon L.J., Gill J.E., Adams M.D., Carreira A.J., Cleary T.H.,  
 CC Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss L.,  
 CC Niernann W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,  
 CC Venter J.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,  
 CC "Sequence and analysis of chromosome 2 of the plant Arabidopsis  
 CC thaliana";  
 CC Nature 402:761-768(1999).  
 CC -1- SIMILARITY: BELONGS TO THE JACALIN LECTIN FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AC004637; AAC28979.1;  
 CC PIR: T02571; T02571.  
 CC HSP: P18674; IJ071.  
 CC InterPro: IPR001229; Jacalin\_lectin.  
 CC Pfam: PF01419; Jacalin; 3.  
 CC Lectin; Repeat; Multigene family.  
 CC KW SEQUENCE 458 AA; 50463 MW; F5G1A413563FAAF8 CRC64;  
 CC -----  
 CC Query Match 91.4%; Score 32; DB 1; Length 458;  
 CC Best Local Similarity 83.3%; Pred. No. 18;  
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 GKGDP 5  
 CC 11111  
 CC DB 214 GKGDP 219  
 CC  
 CC RESULT 7  
 CC ID PAT2\_CAEEL STANDARD: PRT: 1226 AA.  
 CC AC P34446;  
 CC DT 01-FEB-1994 (Rel. 28, Created)  
 CC DT 28-FEB-2003 (Rel. 28, last sequence update)  
 CC DE Integrin alpha pat-2 precursor.  
 CC GN PAT-2 OR F54P2.  
 CC OS Caenorhabditis elegans.  
 CC CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditiformes;  
 CC Rhabditidae; Pelodierinae; Caenorhabditis;  
 CC NCBI\_TaxID=6235;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=Bristol N2;  
 CC MEDLINE=94150718; PubMed=7236196;  
 CC Wilson R., Ainscough R., Anderson K., Raynes C., Berk's M.,  
 CC Benfield J., Burton J., Connel M., Copey T., Cooper J., Coulson A.,  
 CC Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,  
 CC Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
 CC Johnston L., Jones M., Kershaw J., Kirsten J., Laister K.,  
 CC Latreille F., Lightning J., Lloyd C., Mortimore R., O'Callaghan M.,  
 CC Parsons J., Perry C., Rifkin L., Roopra A., Saunders D., Shewmaker R.,  
 CC Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,  
 CC Stalton J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
 CC Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,  
 CC

KA Realdman R.;  
 CC 2.2 kb of contiguous nucleotide sequence from chromosome III of C.  
 CC elease";  
 CC Nature 368:32-38(1994).  
 CC -1- FUNCTION: POSSIBLE ROLE IN CELL-CELL INTERACTIONS (BY SIMILARITY).  
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA PAT-2  
 CC ASSOCIATES WITH BETA PAT-3.  
 CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein (by similarity).  
 CC -1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.  
 CC -1- SIMILARITY: Contains 7 FG-GAP repeats.  
 CC -----  
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 CC -----  
 CC EMBL: I23645; AAK26134.1;  
 CC PIR: S44824; S44824.  
 CC HSP: P05756; IJ072.  
 CC WormPep: F54F2.1; CE00194.  
 CC InterPro: IPR000413; Integrin\_alpha.  
 CC Pfam: PF01839; FG-GAP; 4.  
 CC Pfam: PF00357; Integrin\_A; 1.  
 CC PRINTS: PR01185; INTEGRIN.  
 CC SMART: SM00191; Int\_alpha; 5.  
 CC PROSITE: PS00242; INTEGRIN\_ALPHA; 1.  
 CC Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;  
 CC KW SIGNAL; Repeat; 1 25  
 CC FT CHAIN 26 1226  
 CC FT DOMAIN 26 1154  
 CC FT TRANSMEM 1155 1177  
 CC FT DOMAIN 1178 1226  
 CC FT REPEAT 40 103  
 CC FT REPEAT 120 172  
 CC FT REPEAT 189 243  
 CC FT REPEAT 244 297  
 CC FT REPEAT 300 372  
 CC FT REPEAT 373 433  
 CC FT REPEAT 437 485  
 CC FT CARBOHYD 108 108  
 CC FT CARBOHYD 228 228  
 CC FT CARBOHYD 290 290  
 CC FT CARBOHYD 608 608  
 CC FT CARBOHYD 679 679  
 CC FT CARBOHYD 775 775  
 CC FT CARBOHYD 819 819  
 CC SEQUENCE 1226 AA; 135939 MW; B9189AD75B89901D CRC64;  
 CC  
 CC Query Match 91.4%; Score 32; DB 1; Length 1226;  
 CC Best Local Similarity 83.3%; Pred. No. 54;  
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 GKGDP 5  
 CC 11111  
 CC DB 519 GKGDP 524  
 CC  
 CC RESULT 8  
 CC ID YK1\_YEAST  
 CC AC P40487;  
 CC DT 01-FEB-1995 (Rel. 31, Created)  
 CC DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 CC DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 CC DE Hypothetical 48.3 kDa protein in MCS1-SGA1 intergenic region.  
 CC GN YIL103W.  
 CC OS Saccharomyces cerevisiae (Baker's yeast).  
 CC CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

CC NCBI\_TaxID-4932;  
 CC [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-S2886//AB972;  
 RA PubMed-9189976;  
 RA Churcher C.M., Bowman S., Badcock K., Backler A., Brown E.,  
 RA Chillingworth I., Connor R., Devlin K., Gentles S., Hamlin N.,  
 RA Harris D.E., Horsnell T., Hunt S., Javelis K., Jones M., Lye G.,  
 RA Moulé S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,  
 RA Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.,  
 RA "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome IX,"  
 RT Nature 387:84-87(1997).  
 CC -!- SIMILARITY: TO YEAST DIPHTERIA TOXIN RESISTANCE PROTEIN 2 (PF52),  
 CC TO S.POMBE SPAC13F4.152, SPBC9B.05, TO C.ELEGANS C09G5.2, C1451.5  
 CC AND M.JANASCHII M30483.  
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 CC -----  
 DE EMBL: Z56125; CAA85277.1; -  
 DE PIR: S48469; S48469.  
 DE SGD: S0001365; Y11103W.  
 DE InterPro: IPR002728; Diphtheria toxin.  
 DE Pfam: PF01866; Diphtheria toxin.  
 DE ProDom: PD004399; Diphtheria toxin.  
 DE TrEMBL: T1890322; diphth02.f1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 425 AA; 46310 MW; 25E93852E0376722 CRC64;  
 Query Match 89.6%; Score 31; DP 1; Length 425;  
 Best Local Similarity 83.3%; Pred. NC: 28;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Type 0;  
 QY 1 GRGETP 6  
 DB 415 GRGETP 425  
 111111  
 RESULT 9  
 Y463.SYNY3  
 ID Y463.SYNY3 STANDARD: PRT; 453 AA.  
 AC P73754;  
 DI 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein s1r0863.  
 GN S1R0863.  
 OS Synchocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.  
 OX NCBT\_TaxID-1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97061201; PubMed-8905241;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizi E., Nakamura Y.,  
 RA Miyajima T., Hirose A.M., Sugiura M., Sasamoto S., Kimura T.,  
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nario K.,  
 RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,  
 RA Yamada M., Yasuda M., Tabata S.,  
 RA "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synchocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions,"  
 RL Nucleic Acids Res. 31:109-116(1995).  
 CC -!- SIMILARITY: BELONGS TO THE T1CD/PMBA FAMILY.  
 CC -----  
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 CC -----  
 DE EMBL: L90909; BAA17806.1; -  
 DE PIR: S74845; S74845.  
 DE InterPro: IPR002510; PMBA\_T1CD.  
 DE Pfam: PF01523; PMBA\_T1CD; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 463 AA; 50369 MW; 220173C7C6A42D CRC64;  
 Query Match 88.6%; Score 31; DP 1; Length 463;  
 Best Local Similarity 83.3%; Pred. NC: 31;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGETP 6  
 DB 352 GRGETP 357  
 111111  
 RESULT 10  
 F1NC.CHICK  
 ID F1NC.CHICK STANDARD: PRT; 1255 AA.  
 AC P11722; O90921;  
 DE 01-OCT-1989 (Rel. 12, Created)  
 DE 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Fibronectin (FN) (Fragments).  
 GN FN1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OX Gallus.  
 OX NCBT\_TaxID-9031;  
 RN [1]  
 RP SEQUENCE OF 1-50 FROM N.A.  
 RX MEDLINE-83117850; PubMed-6572007;  
 RA Hirano H., Yamada Y., Sullivan M., de Crombrughe B., Pastan I.,  
 RA Yamada K.M.,  
 RA "Isolation of genomic DNA clones spanning the entire fibronectin  
 RT gene,"  
 RT Proc. Natl. Acad. Sci. U.S.A. 80:46-50(1983).  
 RN [2]  
 RP SEQUENCE OF 51-1256 FROM N.A.  
 RC STRAIN-White leghorn;  
 RA Norton P.A.;  
 RC Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE OF 227-415 FROM N.A.  
 RX MEDLINE-96183658; PubMed-8603103;  
 RA Gehris A.L., Brandli D.W., Lewis S.D., Bennett V.D.;  
 RA "The exon encoding the fibronectin type III-9 repeat is  
 RT constitutively included in the mRNA from chick limb mesenchyme and  
 RT cartilage,"  
 RT Biochim. Biophys. Acta 1311:5-12(1996).  
 RN [4]  
 RP SEQUENCE OF 327-599 FROM N.A.  
 RX MEDLINE-88050950; PubMed-2823899;  
 RA Kubomura S., Obara M., Karasaki Y., Taniguchi H., Gotoh S.,  
 RA Tsuda T., Higashi K., Ohsato K., Harno H.,  
 RA "Genetic analysis of the cell binding domain region of the chicken  
 RT fibronectin gene,"  
 RL Biochim. Biophys. Acta 910:171-181(1987).  
 RN [5]  
 RP SEQUENCE OF 413-1256 FROM N.A.  
 RX MEDLINE-88142820; PubMed-2830457;  
 RA Norton P.A., Hynes R.O.;  
 RA "Alternative splicing of chicken fibronectin in embryos and in normal  
 RT and transformed cells,"  
 RL Mol. Cell. Biol. 7:4297-4307(1987).  
 CC -!- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS  
 CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS  
 CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, DIFFERENTIATION, WOUND

HEALING, AND MAINTENANCE OF CELL SHAPE.  
 -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED  
 VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS  
 TO A LESSER EXTENT HOMODIMERS.  
 -1- ALTERNATIVE PRECURSORS:  
 Event-Alternative splicing: Named isoforms: 1  
 Comment-A number of isoforms are produced. Each of the "extra  
 domain" and the connecting strand 3 are present in some forms of  
 fibronectin and absent in others.  
 Name-1:  
 IsoId=PI1722-1; Sequence displayed:  
 -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE FIBRIN FIBRIN FIBRIN) IS SECRETED  
 BY HEPATOCYTES, CELLULAR FN (MEMBRANE OR CROSS-LINKED MULTIMER)  
 FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS  
 DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.  
 -1- PM: SULFATED (BY SIMILARITY).  
 -1- SIMILARITY: Contains at least 5 fibronectin type III domains.  
 -1- SIMILARITY: Contains at least 5 fibronectin type III domains.  
 -1- SIMILARITY: Contains at least 5 fibronectin type III domains.  
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 -----  
 DR EMBL: V00432; CAA23714.1; -  
 DR EMBL: U21327; AAA73566.1; -  
 DR EMBL: X06533; CAA29781.1; -  
 DR EMBL: M26186; AAA4772.1; ALT\_SEQ.  
 DR EMBL: U20386; AAR01062.1; -  
 DR PIR: A28512; A28512.  
 DR PIR: S71465; S71465.  
 DR HSSP: P02751; 1FNH.  
 DR InterPro: IPR000083; FIBRINCTN.  
 DR InterPro: IPR000361; FN\_III.  
 DR InterPro: IPR000562; FN\_Type\_II.  
 DR InterPro: IPR003962; FN\_III\_subd.  
 DR PRINTS: PR00014; FNTYPE11.  
 DR SMART: SM00058; FN3; 3.  
 DR SMART: SM00060; FN3; 9.  
 DR PROSITE: PS00021; FIBRONECTIN\_2; PARTIAL.  
 DR PROSITE: PS01253; FIBRONECTIN\_1; 2.  
 DR PROSITE: PS01253; FIBRONECTIN\_1; 1.  
 KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;  
 KW Repeat; Sulfation; Alternative splicing.  
 FT NON\_TER 1 1  
 FT NON\_TER 50 51  
 FT DOMAIN 236 509  
 FT DOMAIN 590 961  
 FT DOMAIN 1153 1226  
 FT DOMAIN 1227 1266  
 FT DOMAIN 1267 1306  
 FT DOMAIN 1307 1346  
 FT DOMAIN 1347 1386  
 FT DOMAIN 1387 1426  
 FT DOMAIN 1427 1466  
 FT DOMAIN 1467 1506  
 FT DOMAIN 1507 1546  
 FT DOMAIN 1547 1586  
 FT DOMAIN 1587 1626  
 FT DOMAIN 1627 1666  
 FT DOMAIN 1667 1706  
 FT DOMAIN 1707 1746  
 FT DOMAIN 1747 1786  
 FT DOMAIN 1787 1826  
 FT DOMAIN 1827 1866  
 FT DOMAIN 1867 1906  
 FT DOMAIN 1907 1946  
 FT DOMAIN 1947 1986  
 FT DOMAIN 1987 2026  
 FT DOMAIN 2027 2066  
 FT DOMAIN 2067 2106  
 FT DOMAIN 2107 2146  
 FT DOMAIN 2147 2186  
 FT DOMAIN 2187 2226  
 FT DOMAIN 2227 2266  
 FT DOMAIN 2267 2306  
 FT DOMAIN 2307 2346  
 FT DOMAIN 2347 2386  
 FT DOMAIN 2387 2426  
 FT DOMAIN 2427 2466  
 FT DOMAIN 2467 2506  
 FT DOMAIN 2507 2546  
 FT DOMAIN 2547 2586  
 FT DOMAIN 2587 2626  
 FT DOMAIN 2627 2666  
 FT DOMAIN 2667 2706  
 FT DOMAIN 2707 2746  
 FT DOMAIN 2747 2786  
 FT DOMAIN 2787 2826  
 FT DOMAIN 2827 2866  
 FT DOMAIN 2867 2906  
 FT DOMAIN 2907 2946  
 FT DOMAIN 2947 2986  
 FT DOMAIN 2987 3026  
 FT DOMAIN 3027 3066  
 FT DOMAIN 3067 3106  
 FT DOMAIN 3107 3146  
 FT DOMAIN 3147 3186  
 FT DOMAIN 3187 3226  
 FT DOMAIN 3227 3266  
 FT DOMAIN 3267 3306  
 FT DOMAIN 3307 3346  
 FT DOMAIN 3347 3386  
 FT DOMAIN 3387 3426  
 FT DOMAIN 3427 3466  
 FT DOMAIN 3467 3506  
 FT DOMAIN 3507 3546  
 FT DOMAIN 3547 3586  
 FT DOMAIN 3587 3626  
 FT DOMAIN 3627 3666  
 FT DOMAIN 3667 3706  
 FT DOMAIN 3707 3746  
 FT DOMAIN 3747 3786  
 FT DOMAIN 3787 3826  
 FT DOMAIN 3827 3866  
 FT DOMAIN 3867 3906  
 FT DOMAIN 3907 3946  
 FT DOMAIN 3947 3986  
 FT DOMAIN 3987 4026  
 FT DOMAIN 4027 4066  
 FT DOMAIN 4067 4106  
 FT DOMAIN 4107 4146  
 FT DOMAIN 4147 4186  
 FT DOMAIN 4187 4226  
 FT DOMAIN 4227 4266  
 FT DOMAIN 4267 4306  
 FT DOMAIN 4307 4346  
 FT DOMAIN 4347 4386  
 FT DOMAIN 4387 4426  
 FT DOMAIN 4427 4466  
 FT DOMAIN 4467 4506  
 FT DOMAIN 4507 4546  
 FT DOMAIN 4547 4586  
 FT DOMAIN 4587 4626  
 FT DOMAIN 4627 4666  
 FT DOMAIN 4667 4706  
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FT DOMAIN 568 557 FIBRONECTIN TYPE-III (EXTRA DOMAIN).  
 FT DOMAIN 658 749 FIBRONECTIN TYPE-III.  
 FT DOMAIN 750 838 FIBRONECTIN TYPE-III.  
 FT DOMAIN 839 929 FIBRONECTIN TYPE-III.  
 FT DOMAIN 930 1264 CONNECTING STRAND 3 (CS-3) (V REGION).  
 FT DOMAIN 1265 1143 FIBRONECTIN TYPE-III.  
 FT DOMAIN 1155 1199 FIBRONECTIN TYPE-III.  
 FT DOMAIN 1200 1243 FIBRONECTIN TYPE-III.  
 FT DOMAIN 1245 1287 FIBRONECTIN TYPE-III.  
 FT DISULFID 1157 1186 BY SIMILARITY.  
 FT DISULFID 1184 1196 BY SIMILARITY.  
 FT DISULFID 1202 1229 BY SIMILARITY.  
 FT DISULFID 1227 1249 BY SIMILARITY.  
 FT DISULFID 1247 1270 BY SIMILARITY.  
 FT DISULFID 1268 1284 BY SIMILARITY.  
 FT DISULFID 1320 1320 INTERCHAIN (WITH 1324 OF OTHER CHAIN) (BY SIMILARITY).  
 FT DISULFID 1324 1324 INTERCHAIN (WITH 1320 OF OTHER CHAIN) (BY SIMILARITY).  
 FT SITE 461 463 CELL ATTACHMENT SITE.  
 FT CARBOHYD 89 89 N-LINKED (GLCNAC...) (POTENTIAL)  
 SQ SEQUENCE 1328 AA: 145037 MW: 631567966ALDIET4 CRO64;  
 Query Match 85.6%; Score 31; DB 1; Length 1328;  
 Host Local Similarity 63.1%; Pred. No. 98;  
 Matches 5; Conservative 13; Mismatches 0; Gaps 0;  
 QY 1 GRAFT 6  
 D5 460 GGRNP 465  
 ID FINE BOVIN STANDARD; PRI: 2265 AA.  
 AC P07589;  
 DT 01-APR-1988 (Sci. 37, Created;  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Fibronection (FN).  
 GN FN1.  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 CX NCBI\_TaxId=9913;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=87054047; PubMed=3780752;  
 RA Skorstengaard K., Jensen M.S., Sahl P., Petersen T.E., Magnusson S.;  
 RT "Complete primary structure of bovine plasma fibronection";  
 RL Eur. J. Biochem. 161:441-453(1986).  
 RN [2]  
 RP PARTIAL SEQUENCE.  
 RX MEDLINE=83117805; PubMed=6218503;  
 RA Petersen T.E., Thorgersen H.C., Skorstengaard K., Vibe-Pedersen K.,  
 RA Sahl P., Sottrup-Jensen L., Magnusson S.;  
 RT "Partial primary structure of bovine plasma fibronection: three types  
 of internal homology";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:137-141(1983).  
 RN [3]  
 RP SEQUENCE OF 2170-2265 FROM N.A.  
 RX MEDLINE=83221567; PubMed=6304699;  
 RA Kornblitt A.R., Vibe-Pedersen K., Baralle F.E.;  
 RT "Isolation and characterization of cDNA clones for human and bovine  
 fibronectins";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3218-3222(1983).  
 CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPONENTS  
 INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS  
 ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND  
 HEALING, AND MAINTENANCE OF CELL SHAPE.  
 CC -1- SURUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED  
 VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;  
 TO A LESSER EXTEND HOMODIMERS.  
 -1- ALTERNATIVE PRODUCTS:  
 Event-Alternative splicing: Named isoforms=1;  
 Comment=A number of isoforms are produced. Each of the "extra  
 domain" and the connecting strand 3 are present in some forms of  
 fibronectin and absent in others;  
 Name=1;  
 IsoId=P07589-1; Sequence=Displayed;  
 -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED  
 BY HEPATOCYTES, CELLULAR FN (OLIGOMERIC OR CROSS-LINKED MULTIMERIC  
 FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS  
 DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.  
 -1- PTM: SULFATED (BY SIMILARITY).  
 -1- SIMILARITY: Contains 12 fibronectin type I domains.  
 -1- SIMILARITY: Contains 2 fibronectin type III domains.  
 -1- SIMILARITY: Contains 15 fibronectin type III domains.  
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 the European Bioinformatics Institute. There are no restrictions on its  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 FMBL: K09800; AAA30521.2;  
 FTR: A26452; FNBO.  
 HSSP: P0751; 2FN2.  
 InterPro: IPR004209; EGF-like.  
 InterPro: IPR003083; Fibrinectin.  
 InterPro: IPR003961; FN-III.  
 InterPro: IPR000562; FN\_Type-III.  
 InterPro: IPR003962; FNIII\_sulf.  
 Pfam: PF00039; fn1; 12.  
 Pfam: PF00040; fn2; 2.  
 Pfam: PF00041; fn3; 15.  
 PRINTS: PR00013; FNTYPEIII.  
 PRINTS: PR00014; FNTYPEIII.  
 PRODOM: PD000995; FN\_Type-III; 2.  
 SMART: SMC0058; FN1; 12.  
 SMART: SMC0059; FN2; 2.  
 SMART: SMC0060; FN3; 14.  
 PROSITE: PS00022; EGF\_1; 2.  
 PROSITE: PS00023; FIBRONECTIN\_2; 2.  
 PROSITE: PS01253; FIBRONECTIN\_1; 12.  
 Glycoprotein; Plasma; Heparin-binding; Acute phase; Phosphorylation;  
 Sulfation; Cell adhesion; Repeat; Alternative splicing;  
 Pyroglutamate carboxylic acid.  
 MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT DOMAIN 21 241 FIBRIN- AND HEPARIN-BINDING 1.  
 FT DOMAIN 277 577 COLLAGEN-BINDING.  
 FT DNA\_BIND 876 1141  
 FT DOMAIN 1236 1509 CELL-ATTACHMENT.  
 FT DOMAIN 1600 1870 HEPARIN-BINDING 2.  
 FT DOMAIN 1991 2216 FIBRIN-BINDING 2.  
 FT DOMAIN 19 59 FIBRONECTIN TYPE-1 1.  
 FT DOMAIN 64 107 FIBRONECTIN TYPE-1 2.  
 FT DOMAIN 108 151 FIBRONECTIN TYPE-1 3.  
 FT DOMAIN 153 197 FIBRONECTIN TYPE-1 4.  
 FT DOMAIN 198 242 FIBRONECTIN TYPE-1 5.  
 FT DOMAIN 275 314 FIBRONECTIN TYPE-1 6.  
 FT DOMAIN 314 373 FIBRONECTIN TYPE-1 1.  
 FT DOMAIN 374 438 FIBRONECTIN TYPE-1 2.  
 FT DOMAIN 437 480 FIBRONECTIN TYPE-1 7.  
 FT DOMAIN 485 527 FIBRONECTIN TYPE-1 8.  
 FT DOMAIN 528 571 FIBRONECTIN TYPE-1 9.  
 FT DOMAIN 578 669 FIBRONECTIN TYPE-1 1.  
 FT DOMAIN 688 778 FIBRONECTIN TYPE-1 2.  
 FT DOMAIN 779 874 FIBRONECTIN TYPE-1 3.  
 FT DOMAIN 875 964 FIBRONECTIN TYPE-1 4.  
 FT DOMAIN 965 1054 FIBRONECTIN TYPE-1 5.  
 FT DOMAIN 1055 1141 FIBRONECTIN TYPE-1 6.  
 FT DOMAIN 1142 1234 FIBRONECTIN TYPE-1 7.

FT	DOMAIN	1235	1325	FIBRONECTIN TYPE-111 A.	FN	Fibronection precursor (FN) (Cold-insoluble globulin) (CIG).
FT	DOMAIN	1326	1475	FIBRONECTIN TYPE-111 B.	FN	FN1 OR FN.
FT	DOMAIN	1416	1504	FIBRONECTIN TYPE-111 C.	S	Homo sapiens (Human).
FT	DOMAIN	1510	1599	FIBRONECTIN TYPE-111 D.	S	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
FT	DOMAIN	1600	1631	FIBRONECTIN TYPE-111 E.	OC	Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.
FT	DOMAIN	1692	1733	FIBRONECTIN TYPE-111 F.	OX	NCBI_taxid-9606;
FT	DOMAIN	1781	1829	FIBRONECTIN TYPE-111 G.	OX	[1]
FT	DOMAIN	1821	1900	CONNECTING STRAND 3 (CS-3) (V FIBRONECTIN).	EP	SEQUENCE OF 3-38 FROM N.A.
FT	DOMAIN	1982	2061	FIBRONECTIN TYPE-111 H.	FX	MEDLINE-87030890; PubMed-370189;
FT	DOMAIN	2083	2127	FIBRONECTIN TYPE-111 I.	KA	Gulman A., Yamada K.M., Kornblith A.R.;
FT	DOMAIN	2128	2170	FIBRONECTIN TYPE-111 J.	ET	"Human fibronectin is synthesized as a pro-peptide-peptide."
FT	DOMAIN	2172	2215	FIBRONECTIN TYPE-111 K.	K2	FEBS Lett. 207:145-148(1986).
FT	SITE	1493	1495	CELL ATTACHMENT SITE	KN	[2]
FT	DISULFID	21	47		EP	SEQUENCE OF 1-49 FROM N.A.
FT	DISULFID	45	56		FX	MEDLINE-8717578; PubMed-3041556;
FT	DISULFID	66	94		KA	Dean D.C., Bowles C.L., Hourcade S.;
FT	DISULFID	92	104		ET	"Cloning and analysis of the promoter region of the human fibronectin gene."
FT	DISULFID	116	118		ET	Proc. Natl. Acad. Sci. U.S.A. 84:1875-1880(1987).
FT	DISULFID	136	148		KN	[3]
FT	DISULFID	153	194		EP	SEQUENCE OF 32-2081 AND 2113-2386 FROM N.A.
FT	DISULFID	182	194		FX	MEDLINE-85284965; PubMed-2992939;
FT	DISULFID	200	229		KA	Kornblith A.R., Umezawa K., Vibe-Pedersen K., Baralle F.E.;
FT	DISULFID	227	239		ET	"Primary structure of human fibronectin: differential splicing may generate at least 10 polypeptides from a single gene."
FT	DISULFID	302	311		ET	EMBO J. 4:1755-1759(1985).
FT	DISULFID	329	355		KN	[4]
FT	DISULFID	343	370		KN	SEQUENCE OF 373-2081 AND 2113-2386 FROM N.A.
FT	DISULFID	383	415		RP	MEDLINE-8427258; PubMed-6462919;
FT	DISULFID	404	430		RX	Kornblith A.R., Vibe-Pedersen K., Baralle F.E.;
FT	DISULFID	439	457		RA	"Human fibronectin: cell specific alternative mRNA splicing generates polypeptide chains differing in the number of internal repeats."
FT	DISULFID	465	477		ET	Nucleic Acids Res. 12:5853-5866(1984).
FT	DISULFID	487	514		ET	[5]
FT	DISULFID	512	524		ET	SEQUENCE OF 1594-2386 FROM N.A.
FT	DISULFID	530	558		KN	MEDLINE-85280409; PubMed-2992573;
FT	DISULFID	556	568		RP	Hernard M.P., Kolbe M., Weil D., Chu M.-L.;
FT	DISULFID	2085	2114		RX	"Human cellular fibronectin: comparison of the carboxyl-terminal portion with rat identifies primary structural domains separated by hypervariable regions."
FT	DISULFID	2112	2124		RA	Biochemistry 24:2698-2704(1985).
FT	DISULFID	2130	2157		ET	[6]
FT	DISULFID	2155	2167		ET	SEQUENCE OF 32-290.
FT	DISULFID	2174	2200		KN	MEDLINE-84032463; PubMed-6530202;
FT	DISULFID	2198	2205		RP	Garcia-Pardo A., Pearlstein E., Franciose B.;
FT	DISULFID	2245	2246		ET	"Primary structure of human plasma fibronectin. The 29,000 dalton NH2-terminal domain."
FT	DISULFID	2250	2250		ET	J. Biol. Chem. 258:12670-12674(1983).
FT	MOD_RES	845	845		KN	[7]
FT	MOD_RES	850	850		KN	SEQUENCE OF 309-608, AND COLLAGEN-5INCLIN3.
FT	CARBOHYD	359	359		KN	MEDLINE-87080265; PubMed-3024962;
FT	CARBOHYD	457	457		KA	Owens R.J., Baralle F.E.;
FT	CARBOHYD	511	511		ET	"Mapping the collagen-binding site of human fibronectin by expression in Escherichia coli."
FT	CARBOHYD	646	646		ET	EMBO J. 5:2825-2830(1986).
FT	CARBOHYD	974	974		ET	[8]
FT	CARBOHYD	1213	1213		KN	SEQUENCE OF 1441-1548.
FT	CARBOHYD	1987	1987		KN	MEDLINE-82265604; PubMed-7050098;
FT	CARBOHYD	1943	1943		ET	Pierischbacher M.D., Ruoslahti E., Sandoz J., Lind P., Peterson P.A.;
FT	CARBOHYD	1944	1944		ET	"The cell attachment domain of fibronectin. Determination of the primary structure."
FT	MOD_RES	2263	2263		ET	J. Biol. Chem. 257:9593-9597(1982).
FT	SEQUENCE	2265	2265		KN	[9]
FT	SEQUENCE	2265	2265		KN	SEQUENCE OF 1434-1537 FROM N.A.
FT	SEQUENCE	2265	2265		KN	MEDLINE-83290929; PubMed-6688419;
FT	SEQUENCE	2265	2265		KN	Oldberg A., Linney E., Ruoslahti E.;
FT	SEQUENCE	2265	2265		ET	"Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell attachment domain in human fibronectin."
FT	SEQUENCE	2265	2265		ET	J. Biol. Chem. 258:10193-10196(1983).
FT	SEQUENCE	2265	2265		KN	[10]
FT	SEQUENCE	2265	2265		KN	SEQUENCE OF 1448-1540 FROM N.A.
FT	SEQUENCE	2265	2265		ET	MEDLINE-86111901; PubMed-3003995;
FT	SEQUENCE	2265	2265		ET	Oldberg A., Ruoslahti E.;

Query Match 88.6% Score 31.25 Len 2265

Best Local Similarity 81.3% P-Val 1.4e-02

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 GRGDP 6

|||||

Db 1492 GRGDP 1497

RESULT 13

ID FINE\_HUMAN STANDARD: PKC: 2386 AA.

AC P02751; Q14726; Q9H188;

DT 21-JUL-1986 (Ref. 01, Created);

DT 01-NOV-1997 (Ref. 35, Last sequence update)

DT 15-SEP-2003 (Ref. 42, Last annotation update)

RT \*Evolution of the fibronectin gene. Exon structure of cell attachment  
 RL domain".  
 RN J. Biol. Chem. 261:2113-2116(1986).  
 RN [11]  
 RP SEQUENCE OF 1712-1739 FROM N.A.  
 RX MEDLINE-87026578; PubMed-3021206;  
 RA Sekiguchi K., Kios A.M., Kurachi K., Yoshitake S., Hakomori S.  
 RT \*Human liver fibronectin complementary DNAs: identification of two  
 RT different messenger RNAs possibly encoding the alpha and beta  
 RT subunits of plasma fibronectin".  
 RL Biochemistry 25:4536-4541(1986).  
 RN [12]  
 RP SEQUENCE FROM N.A. (1800-PM 2).  
 RX Schor S.L., Schor A.M., Schneviratne K., Kay R., Ellis J., Bailly E.,  
 SA Clausen J.  
 RT \*Migration stimulating factor (MSF): a novel transcription variant of  
 RT the fibronectin gene".  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBCC databases.  
 RN [13]  
 RP SULFATION.  
 RX MEDLINE-86042625; PubMed-2414772;  
 RA Liu M.C., Yu S., Sy J., Kedman G.M., Lipmann F.  
 RT \*Tyrosine sulfation of proteins from the human hepatoma cell line  
 RT HepG2".  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).  
 RN [14]  
 RP FBLN1-BINDING SITE.  
 RX PubMed-1420349;  
 RA Baibona K., Tran H., Gedrya S., Ingham K.C., Strickland D.K.,  
 RA Argraves W.S.  
 RT \*Fibulin binds to itself and to the carboxyl-terminal heparin-binding  
 RT region of fibronectin".  
 RL J. Biol. Chem. 267:20129-20125(1992).  
 RN [15]  
 RP CHARACTERIZATION OF FIBRIN-BINDING SITE 1.  
 RX MEDLINE-95081153; PubMed-7389359;  
 RA Rostagno A., Williams M.J., Baron M., Campbell I.D., Gold L.L.  
 RT \*Further characterization of the NH2-terminal fibrin-binding site in  
 RT fibronectin".  
 RL J. Biol. Chem. 269:31938-31948(1994).  
 RN [16]  
 RP STRUCTURE BY NMR OF 32-92.  
 RX MEDLINE-96069779; PubMed-7583666;  
 RA Potts J.R., Phan I., Williams M.J., Campbell I.D.  
 RT \*High-resolution structural studies of the factor XIIIa crosslinking  
 RT site and the first type 1 module of fibronectin".  
 RL Nat. Struct. Biol. 2:946-950(1995).  
 RN [17]  
 RP STRUCTURE BY NMR OF 182-275.  
 RX MEDLINE-9444923; PubMed-6308892;  
 RA Williams M.J., Phan I., Harvey T.S., Rostagno A., Gold L.L.,  
 RA Campbell I.D.  
 RT \*Solution structure of a pair of fibronectin type 1 modules with  
 RT fibrin binding activity".  
 RL J. Mol. Biol. 235:1302-1311(1994).  
 RN [18]  
 RP STRUCTURE BY NMR OF 406-464.  
 RX MEDLINE-98179558; PubMed-9514732;  
 RA Sticht H., Pickford A.R., Potts J.R., Campbell I.D.  
 RT \*Solution structure of the glycosylated second type 2 module of  
 RT fibronectin".  
 RL J. Mol. Biol. 276:177-187(1998).  
 RN [19]  
 RP STRUCTURE BY NMR OF 1447-1540.  
 RX MEDLINE-93046665; PubMed-1423622;  
 RA Main A.L., Harvey T.S., Baron M., Boyd H., Campbell I.D.  
 RT \*The three-dimensional structure of the tenth type III module of  
 RT fibronectin: an insight into RGD-mediated interactions".  
 RL Cell 71:671-678(1992).  
 RN [20]  
 RP STRUCTURE BY NMR OF 1447-1540.  
 RX MEDLINE-92162710; PubMed-1111202;  
 RA Baron M., Main A.L., Driscoll P.C., Mardon H.J., Boyd H.

RA Campbell I.D.  
 RT \*1H NMR assignment and secondary structure of the cell adhesion type  
 RL III module of fibronectin".  
 RN Biochemistry 31:2068-2073(1992).  
 RN [21]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1447-1545.  
 RX MEDLINE-94166075; PubMed-8120888;  
 RA Dickinson C.D., Veerapandian B., Dai X.-P., Hamlin R.C., Xuong N.-H.,  
 RA Ruoslahti E., Ely K.R.  
 RT \*Crystal structure of the tenth type III cell adhesion module of  
 RT human fibronectin".  
 RL J. Mol. Biol. 236:1079-1092(1994).  
 RN [22]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 1721-1991.  
 RX MEDLINE-99177162; PubMed-10075919;  
 RA Sharma A., Askari J.A., Humphries M.J., Jones E.Y., Stuart D.L.  
 RT \*Crystal structure of a heparin- and integrin-binding segment of human  
 RT fibronectin".  
 RL EMBO J. 18:1468-1479(1999).  
 CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS  
 CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS  
 CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, ORGANOIZATION, WOUND  
 CC HEALING, AND MAINTENANCE OF CELL SHAPE.  
 CC -1- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced  
 CC variants, connected by 2 disulfide bonds near the carboxyl ends;  
 CC to a lesser extent homodimers. Interacts with FBLN1.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms 2;  
 CC Comment-Additional isoforms seem to exist;  
 CC Name: 1;  
 CC IsoId: P02751-1; Sequence-Displayed;  
 CC Names: 2; Synonyms-MSF-FN70, Migration stimulation factor FN70;  
 CC IsoId: P02751-2; Sequence-VSP\_003255, VSP\_003256, VSP\_003257;  
 CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE D-MERIC FORM) IS SECRETED  
 CC BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC  
 CC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS  
 CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.  
 CC -1- PTM: SULFATED.  
 CC -1- SIMILARITY: Contains 12 fibronectin type I domains.  
 CC -1- SIMILARITY: Contains 4 fibronectin type II domains.  
 CC -1- SIMILARITY: Contains 16 fibronectin type III domains.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC Query Match 88.6%; Score 31; DB 1; Length 2386;  
 CC Best Local Similarity 83.3%; Prod. No. 1.9e+02;  
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC Qy 1 GRGDTP 6  
 CC |---|  
 CC Eb 1523 GRGDSP 1528  
 CC  
 CC RESULT 14  
 CC FINC\_MOUSE  
 CC ID FINC\_MOUSE STANDARD; PRT: 2477 AA.  
 CC AC P11276; O61567; O61568; O61569; O64233;  
 CC DT 01-JUL-1989 (Rel. 11, Created)  
 CC DE 01-NOV-1997 (Rel. 35, Last sequence update)  
 CC DI 15-SEP-2003 (Rel. 42, Last annotation update)  
 CC OE Fibronectin precursor (FN) (fragments).  
 CC GN FNI.  
 CC OS Mus musculus (Mouse).  
 CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]



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FT DOMAIN 2282 2281 CONNECTING STRAND 4 (CS-1) (V REGION)
FT DOMAIN 2282 2281 FIBRONECTIN TYPE-III 17
FT DOMAIN 2282 2281 FIBRONECTIN TYPE-III 17
FT DOMAIN 2282 2281 FIBRONECTIN TYPE-III 17
FT DOMAIN 2282 2281 FIBRONECTIN TYPE-III 17
FT SITE 163 161 CELL ATTACHMENT SITE
FT SITE 2182 2181 CELL ATTACHMENT SITE
FT DISULFID 561 559 BY SIMILARITY
FT DISULFID 587 599 BY SIMILARITY
FT DISULFID 2296 2325 BY SIMILARITY
FT DISULFID 2323 2335 BY SIMILARITY
FT DISULFID 2341 2368 BY SIMILARITY
FT DISULFID 2366 2378 BY SIMILARITY
FT DISULFID 2385 2409 BY SIMILARITY
FT DISULFID 2407 2424 BY SIMILARITY
FT DISULFID 2458 2458 INTERCHAIN (WITH 2462 OF OTHER CHAIN)
FT DISULFID 2462 2462 INTERCHAIN (WITH 2458 OF OTHER CHAIN)
FT CARBOHYD 1006 1006 N-LINKED (GLUCNA) (POTENTIAL)
FT CARBOHYD 1243 1243 N-LINKED (GLUCNA) (POTENTIAL)
FT CARBOHYD 1290 1290 N-LINKED (GLUCNA) (POTENTIAL)
FT CARBOHYD 2198 2198 N-LINKED (GLUCNA) (POTENTIAL)
FT MOD_RES 2475 2475 PHOSPHORYLATION (BY SIMILARITY)
FT CONFLICT 2440 2440 N -> T (IN REV. 5)
FT STRAND 1455 1459
FT STRAND 1464 1467
FT STRAND 1477 1484
FT TURN 1485 1485
FT STRAND 1492 1495
FT TURN 1496 1499
FT STRAND 1502 1505
FT STRAND 1512 1521
FT STRAND 1526 1526
FT STRAND 1536 1536
FT STRAND 1542 1550
FT TURN 1551 1552
FT STRAND 1553 1553
FT STRAND 1567 1572
FT TURN 1577 1578
FT STRAND 1592 1586
FT STRAND 1592 1596
FT TURN 1603 1601
FT STRAND 1603 1611

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Query Match 82.6% Score 31; DB 1; Length 2477;

Best Local Similarity 83.3% Pred. No. 136-02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GRGCTP 6

DB 1613 GRGCTP 1628

RESULT 15

FINC\_RAT

AC P04937; STANDARD; PRT: 2477 AA.

DT 13-NOV-1987 (Rev. 05, Created)

DT 01-AUG-1990 (Rev. 16, Last sequence update)

DE 15-SEP-2003 (Rev. 42, Last annotation update)

DE Fibronectin precursor (FN).

GN FN1

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-Fischer; TISSUE-Liver;

RA MEDLINE=88054950; PubMed=2445560;

RA Schwarzbauer J.E., Patel R.S., Fonda D., Hynes R.O.;

RT "Multiple sites of alternative splicing of the rat fibronectin gene

transcript."

RL EMBL J. 6:2573-2580(1987).

```

RN [2]
RP SEQUENCE OF 1-139 AND 2382-2477 FROM N.A.
RC STRAIN-Fischer; TISSUE-Liver;
RX MEDLINE=88054950; PubMed=2445560;
RA Patel R.S., Odermatt E., Schwarzbauer J.E., Hynes R.O.;"
RT "Organization of the fibronectin gene provides evidence for exon
RI shuffling during evolution.";
RL EMBL J. 6:2565-2572(1987).
RN [3]
RP SEQUENCE OF 1586-2477 FROM N.A.
RC MEDLINE=84082067; PubMed=8317187;
RA Schwarzbauer J.E., Tamkun J.W., Lemischka I.R., Hynes R.O.;"
RT "Three different fibronectin mRNAs arise by alternative splicing
RI within the coding region.";
RL Cell 35:421-431(1983).
CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPCNIZATION, WOUND
CC HEALING, AND MAINTENANCE OF CELL SHAPE.
CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
CC TO A LESSER EXTENT HOMODIMERS.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms 4;
CC Comment-Each of the "extra domain" and the connecting strand 3
CC are present in some forms of fibronectin and absent in others;
CC Name-1;
CC IsoId=P04937-1; Sequence-Displayed;
CC Name-2; Synonyms-FNIII-13-less;
CC IsoId=P04937-2; Sequence-VSP_003258;
CC Name-3; Synonyms-Lambda-RIF4-5;
CC IsoId=P04937-3; Sequence-VSP_003259;
CC Name-4; Synonyms-Lambda-RIF6;
CC IsoId=P04937-4; Sequence-VSP_003260;
CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM); IS SECRETED
CC BY HEPATOCTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
CC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
CC -1- PTM: SULFATED (BY SIMILARITY).
CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 17 fibronectin type III domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb.sib.ch/announce/
CC or send an email to licensewiz@sib.ch).
CC -----
CC EMBL; X15906; CAA34020.1; -
CC EMBL; L29191; AAA41166.1; -
CC EMBL; L00191; AAA41166.1; JOINED.
CC EMBL; L29191; AAA41167.1; -
CC EMBL; L00191; AAA41167.1; JOINED.
CC EMBL; L29191; AAA41168.1; -
CC EMBL; L00191; AAA41168.1; JOINED.
CC EMBL; X05831; CAA29278.1; -
CC EMBL; X05833; CAA29279.1; -
CC EMBL; X05833; CAA29280.1; -
CC EMBL; X05834; CAA29281.1; -
CC PIR; S14428; S14428.
CC HSP; P02751; IPR8.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR000083; Fibrnctnl.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR000562; FN_Type_II.
CC InterPro; IPR003962; FNIII_subd.
CC Pfam; PF000039; fn1; 12.
CC Pfam; PF000040; fn2; 2.
CC Pfam; PF000041; fn3; 17.
CC PRINTS; PR00013; FNTYPEII.

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Search completed: September 16, 2003, 18:17:00  
 Job time : 14 secs

SeqCore version: 5.1.1.6  
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OM protein - protein search, using sw model

Run on: September 16, 2003, 18:14:22 : Search time 34 seconds  
(without alignments)  
46,919 Million cell updates/sec

Title: US-09-780-612A-1  
Perfect score: 35  
Sequence: 1 GRGDTG 6

Scoring table: BLOSUM62  
Gapop 10.0 : Gapext 0.5

Searched: 530525 seqs, 254052604 residues

Total number of hits satisfying chosen parameters: 530525

Minimum DB seq length: 6  
Maximum DB seq length: 2600000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTRMAL\_23:\*

- 1: SP archaea:\*
- 2: SP bacteria:\*
- 3: SP fungi:\*
- 4: SP human:\*
- 5: SP invertebrate:\*
- 6: SP mammal:\*
- 7: SP plant:\*
- 8: SP archaea:\*
- 9: SP plant:\*
- 10: SP plant:\*
- 11: SP rodent:\*
- 12: SP virus:\*
- 13: SP vertebrate:\*
- 14: SP unclassified:\*
- 15: SP virus:\*
- 16: SP bacteriap:\*
- 17: SP archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	354	5 Q9B110	Q9B110 Bombyx mori
2	35	100.0	450	16 Q9AA55	Q9AA55 Caulobacter
3	35	100.0	490	11 Q9CSK5	Q9CSK5 Mus musculus
4	35	100.0	496	11 Q9ET34	Q9ET34 Rattus norvegicus
5	35	100.0	1209	5 Q8T8C0	Q8T8C0 Bombyx mori
6	32	91.4	458	10 Q8TAD2	Q8TAD2 Arabidopsis
7	32	91.4	605	15 Q8YKQ0	Q8YKQ0 Anabaena sp
8	31	88.6	23	4 Q9UC00	Q9UC00 Homo sapiens
9	31	88.6	85	2 Q9E2D2	Q9E2D2 Rhizobium m
10	31	88.6	185	8 Q8HUM8	Q8HUM8 Woodwardia
11	31	88.6	185	6 Q8HUM7	Q8HUM7 Woodwardia
12	31	88.6	185	3 Q8HUM2	Q8HUM2 Woodwardia
13	31	88.6	208	16 Q8ZK28	Q8ZK28 Rhizobium m
14	31	88.6	218	4 Q8N290	Q8N290 Homo sapiens
15	31	88.6	275	16 Q92BA3	Q92BA3 Rhizobium m
16	31	88.6	293	6 Q9XSG0	Q9XSG0 Corynebacte

17	31	88.6	301	11 Q8C0C1	Q8C0C1 Mus musculus
18	31	88.6	363	11 Q8CC85	Q8CC85 Mus musculus
19	31	88.6	399	17 Q9HQ14	Q9HQ14 Halobacteri
20	31	88.6	407	8 Q8SGBC	Q8SGBC Micropterus
21	31	88.6	438	2 Q9X2S7	Q9X2S7 Vibrio chol
22	31	88.6	438	16 Q9KNL9	Q9KNL9 Vibrio chol
23	31	88.6	441	17 Q9HQN2	Q9HQN2 Halobacteri
24	31	88.6	515	16 Q8X6B0	Q8X6B0 Escherichia
25	31	88.6	515	16 Q8FKR9	Q8FKR9 Escherichia
26	31	88.6	562	4 Q8NC49	Q8NC49 Homo sapien
27	31	88.6	589	13 Q8QVY3	Q8QVY3 Brachydanio
28	31	88.6	606	5 Q18869	Q18869 Caenorhabdi
29	31	88.6	618	17 Q8TYO5	Q8TYO5 Methacopyru
30	31	88.6	659	10 Q8GMX7	Q8GMX7 Arabidopsis
31	31	88.6	686	11 Q8CS85	Q8CS85 Mus musculus
32	31	88.6	686	11 Q8BM24	Q8BM24 Mus musculus
33	31	88.6	691	10 Q8M334	Q8M334 Arabidopsis
34	31	88.6	1105	5 Q9VX44	Q9VX44 Drosophila
35	31	88.6	1169	5 Q9VX45	Q9VX45 Drosophila
36	31	88.6	1174	5 Q8MOX9	Q8MOX9 Drosophila
37	33	88.6	2478	13 Q93406	Q93406 Brachydanio
38	30	85.7	138	15 Q9Z277	Q9Z277 Chimpanzee
39	30	85.7	144	11 Q8C3E1	Q8C3E1 Mus musculus
40	30	85.7	161	11 Q9CV77	Q9CV77 Mus musculus
41	30	85.7	181	16 Q9ZK15	Q9ZK15 Rhizobium m
42	30	85.7	192	16 Q8NPQ8	Q8NPQ8 Corynebacte
43	30	85.7	207	16 Q8N171	Q8N171 Corynebacte
44	30	85.7	231	5 Q9G016	Q9G016 Caenorhabdi
45	30	85.7	247	3 Q9C1R3	Q9C1R3 Emeritella

ALIGNMENTS

RESULT 1  
Q9C1R3  
ID: Q9C1R3 PRELIMINARY: PRT: 354 AA.  
AC: Q9C1R3  
DE: 31-JUN-2001 (TrEMBLrel. 17, Created)  
DE: 31-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DE: 31-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE: Inducible nitric oxide synthase-like protein (INOS-LP)  
DE: (Fragment).  
GN: INOS-LP.  
OS: Bombyx mori (Silk moth).  
OC: Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC: Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
OC: Bombycidae; Bombyx.  
OX: NCBI\_TaxID=7091;  
RN: [1]  
RP: SEQUENCE FROM N. A.  
RA: Yang J., Taitai K., Yanakawa M.;  
RC: "Inducible nitric oxide synthase-like protein (INOS-LP) cDNA."  
RC: Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
DR: EMBL: AB017521; BAB33296.1; -;  
DR: HSSP: P29477; INOC.  
DR: InterPro: IPR004030; NO\_synthase.  
DR: Pfam: PF02898; NO\_synthase; -;  
DR: PROSITE: PS00001; NOS; 1.  
FT: NON\_TER 354 354  
SQ: SEQUENCE 354 AA; 40804 MW; 8D75BA887B739F9A CRC64;

Query Match 100.0%; Score 35; DB 5; Length 354;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 6; Conservative C; Mismatches 0; Indels 0; Gaps 0;

Qy : GRGDTG 6  
      |||||

Dy : :09 GRGDTG 114

RESULT 2  
Q9AA55

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ID Q9AA55 PRELIMINARY: PRT: 450 AA.
AC Q9AA55;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Multidrug resistance protein, putative
GN CC0751.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=55892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19689 / CR15;
RC MEDLINE=21173598; PubMed=11256447;
RA Eisen J., Heidelberg J.F., Alley M.K., Chla H., Mallick D.B., Fly B.,
RA Potocka L., Nelson W.C., Newton A., Stephens J., Peadar D.H.,
RA DeBoy R.T., Dodson R., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Smit M.B., Khouri R., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RA "Complete genome sequence of Caulobacter crescentus";
RA Proc. Natl. Acad. Sci. USA. 98:4336-4341;2001;
RL EMBL: A6005751; AAK22736.1;
RG TIGR: CC0751;
DR InterPro: IPR007114; MFS;
DR InterPro: IPR001958; TCR_TOLA;
DR PRINTS: PR01035; TCR_TOLA;
DR PROSITE: PS03850; MFS: 1;
DR Complete proteome.
SK SEQUENCE 450 AA; 46965 MW; 6577B79F6F5892 CRC64;

Query Match 100.0%; Score 35; DB 16; Length 450;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6
DB 220 GRGDTP 225
|||||

RESULT 3
Q9CSK5 PRELIMINARY: PRT: 490 AA.
AC Q9CSK5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 2810001M03RIK protein (Fragment).
GN SF3B1 OR 2810001M03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57Bl/6J; TISSUE=Embryo;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshida M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosaka H., Kondo S., Yamagata S.,
RA Saito T., Okazaki Y., Gotohori T., Hono H., Kasukawa T., Saifu M.,
RA Kadota K., Matsuda H.A., Ashburner M., Ratalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glisic C., Kirg B., Kishiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido T., Pusate G., Gackebush J.,
RA Schriml L.M., Staehli F., Suzuki R., Tomita M., Wagner L., Washie I.,
RA Sakai K., Oxido T., Furuno M., Aono H., Balkarali F., Bartsch G.,
RA Blake J., Seifell J., de Bojana N., Carinci P., de Benedic M.F.,
RA Brownstein M.J., Rult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee K.H.,
RA Lyons P., Marconcioni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordore P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

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RA Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz G., Whittaker C., Wilming L.,
RA Wyoshaw-Boris A., Yoshida K., Hasegawa Y., Kowaji H., Kozuski S.,
RA Hayashizaki Y.;
RA "functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001);
DR EMBL: AK012632; BAE28369.1;
DR MCD: MCD:1932339; Sfl3b1.
FT NON_TER 490 490
SQ SEQUENCE 490 AA; 53634 MW; F326E5C92B707F3 CRC64;

Query Match 100.0%; Score 35; DB 11; Length 490;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6
DB 269 GRGDTP 274
|||||

RESULT 4
Q9ET34 PRELIMINARY: PRT: 496 AA.
AC Q9ET34;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Spliceosomal protein SAPI55 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Costain W.J., Mishra R.K.;
RA "Identification and cloning of rat SAPI55 homolog.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF260435; AAG01404.1;
FT NON_TER 496 496
SQ SEQUENCE 496 AA; 54496 MW; 5175C3E304272587 CRC64;

Query Match 100.0%; Score 35; DB 11; Length 496;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDTP 6
DB 269 GRGDTP 274
|||||

RESULT 5
Q9TRC9 PRELIMINARY: PRT: 1239 AA.
AC Q9TRC9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Nitric oxide synthase.
GN BMNOS.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Lepidoptera;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RA Imamura M., Yang J., Yamakawa M.;
RA "cDNA cloning, characterization and gene expression of nitric oxide
RA synthase from the silkworm, Bombyx mori.";
RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB071182; BAB58316.1;
FT InterPro: IPR003097; FAD_binding.

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DR InterPro: IPR001226; Flavodoxin.  
 DR InterPro: IPR004030; NO-synthase.  
 DR InterPro: IPR001433; Oxred\_FAD/NAC(P).  
 DR Pfam: PF00667; FAD\_binding\_1; 1.  
 DR Pfam: PF00258; flavodoxin; 1.  
 DR Pfam: PF00179; NAD\_binding\_1; 1.  
 DR Pfam: PF02898; NO-synthase; 1.  
 DR PROSITE: PS00601; NOS; 1.  
 SQ SEQUENCE 1209 AA: 137506 MW: 52A74E04B1202E2C CRC64:  
 Query Match 100.0%; Score 35; DB 5; Length 1209;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGDTP 6  
 DB 109 GRGDTP 114  
 DB 109 GRGDTP 114

RESULT 6  
 Q8LBD2 ID Q8LBD2 PRELIMINARY: PRT; 458 AA.  
 AC Q8LBD2;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created);  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update);  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);  
 DE Putative myrosinase-binding protein.  
 DE Arabidopsis thaliana (Mouse ear cross).  
 DE Eukaryota; Viridiplantae; Streptophyta;  
 OC Spermatophyta; Malvaceae; Brassicaceae; Arabidopsis.  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NCBI\_TaxID:3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Haas R.J., Volkovskiy N., Town C.D., Cronkham M., Alexandrov K.,  
 RA Feldmann K.A., Flavell K.R., White G., Salzberg S.L.;  
 RT "Full-length messenger RNA sequences greatly improve genome  
 RI annotation.";  
 RL Genome Biol. 3:3-0(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Brover V., Cronkham M., Alexandrov N., Lu Y. P., Flavell K.,  
 RA Feldmann K.;  
 RI "Full-length cDNA from Arabidopsis thaliana.";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/CCDB databases.  
 DR EMBL: AY067231; AAM54834.1; 1.  
 DR InterPro: IPR001229; Jacalin\_lectin.  
 DR Pfam: PF01419; Jacalin; 3.  
 SQ SEQUENCE 458 AA: 50376 MW: 6D3F10FB31B83C5 CRC64:  
 Query Match 91.4%; Score 32; DB 10; Length 458;  
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGDTP 6  
 DB 214 GRGDTP 213

RESULT 7  
 Q8YKQO ID Q8YKQO PRELIMINARY: PRT; 456 AA.  
 AC Q8YKQO;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created);  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update);  
 DT 01-MAR-2003 (TrEMBLrel. 21, Last annotation update);  
 DE Hypothetical protein A17243.  
 GN ALR7243.  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 NCBI\_TaxID:103690;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.  
 RX MEDLINE-2595285; PubMed-11759840;  
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz J., Sasamoto S.,  
 RA Watanabe A., Iriuchi M., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakazaki N., Shirao S., Sugimoto M., Takazawa M., Yamada M.,  
 RA Yasuda M., Tabata S.;  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing  
 RT cyanobacterium Anabaena sp. strain PCC 7120.";  
 RL DNA Res. 8:205-213(2003).  
 DR EMBL: AF003600; BAB78327.1; 1.  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 10.  
 DR SMART: SM00248; ANK; 9.  
 DR PROSITE: PS50088; ANK\_REPEAT; 3.  
 DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE: PS03000; SRP54; 1.  
 KW Plasmid; Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 606 AA: 66738 MW: 54A81020A5822E82 CRC64:  
 Query Match 91.4%; Score 32; DB 16; Length 606;  
 Best Local Similarity 83.3%; Pred. No. 3.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGDTP 6  
 DB 120 GRGDTP 125

RESULT 8  
 Q9HDC2 ID Q9HDC2 PRELIMINARY: PRT; 21 AA.  
 AC Q9HDC2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created);  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update);  
 DE Enhancement of wound HEALING process.  
 DE Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95130623; PubMed-7829572;  
 RA Pierschbacher M.D., Poirak J.W., Craig W.S., Tschopp J.P.,  
 RA Sipes N.J., Harper J.R.;  
 RL J. Cell. Biochem. 56:150-154(1994).  
 SQ SEQUENCE 23 AA: 2268 MW: CE736997B97389 CRC64:  
 Query Match 88.6%; Score 31; DB 4; Length 23;  
 Best Local Similarity 83.3%; Pred. No. 18;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGDTP 6  
 DB 1 GRGDTP 6

RESULT 9  
 Q9E2D2 ID Q9E2D2 PRELIMINARY: PRT; 86 AA.  
 AC Q9E2D2;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created);  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update);  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update);  
 DE Hypothetical 9.1 kDa protein.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Sinorhizobium.  
 NCBI\_TaxID:382;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-RU11/001;  
 Muschler P.F.J., Foster C.;  
 "Isolation of mcp genes from *Sinorhizobium meliloti*."  
 Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.  
 ERL EMBL: AF208190; AAC37856.1; -;  
 RRL Hypothetical protein.  
 KKW  
 SQ SEQUENCE 86 AA; 9128 MW; 87035856B176D32A CRC64;  
 Query Match 88.6%; Score 31; DB 8; Length 185;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGTP 6  
 I I I I I  
 DB 35 GRGSP 40

RESULT 10  
 Q8HUM8 PRELIMINARY: PRT: 185 AA.  
 AC Q8HUM8;  
 DI 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Ribosomal protein small subunit 4 (Fragment).  
 RPS4.  
 OS Woodwardia fimbriata.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OOC Filicophyta; Filicopsida; Filicales; Blechnaceae; Woodwardia.  
 OX NCBI\_TaxID=29664;  
 RX [1]  
 SEQUENCE FROM N.A.  
 RA Cranfill R., Kato M.;  
 RT "Phylogenetics, Biogeography, and Classification of the woodwardioid  
 ferns (Blechnaceae)."  
 RRL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.  
 RLL EMBL: AF533859; AAN34638.1; -;  
 RRR Chloroplast.  
 KKW  
 SQ SEQUENCE 185 AA; 20723 MW; D8795983F5283F9E CRC64;  
 Query Match 88.6%; Score 31; DB 8; Length 185;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGTP 6  
 I I I I I  
 DB 2 GRGTP 7

RESULT 11  
 Q8HUM7 PRELIMINARY: PRT: 185 AA.  
 AC Q8HUM7;  
 DI 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Ribosomal protein small subunit 4 (Fragment).  
 RPS4.  
 OS Woodwardia fimbriata.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OOC Filicophyta; Filicopsida; Filicales; Blechnaceae; Woodwardia.  
 OX NCBI\_TaxID=120727;  
 RX [1]  
 SEQUENCE FROM N.A.  
 RA Cranfill R., Kato M.;  
 RT "Phylogenetics, Biogeography, and Classification of the woodwardioid  
 ferns (Blechnaceae)."  
 RRL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.  
 RLL EMBL: AF533860; AAN34639.1; -;  
 RRR Chloroplast.

FI NON\_TER 1 1  
 SQ SEQUENCE 185 AA; 20699 MW; 9E9D177082010457 CRC54;  
 Query Match 88.6%; Score 31; DB 8; Length 185;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGTP 6  
 I I I I I  
 DB 2 GRGTP 7

RESULT 12  
 Q8HUM2 PRELIMINARY: PRT: 185 AA.  
 AC Q8HUM2;  
 DI 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Ribosomal protein small subunit 4 (Fragment).  
 RPS4.  
 OS Woodwardia spinulosa.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OOC Filicophyta; Filicopsida; Filicales; Blechnaceae; Woodwardia.  
 OX NCBI\_TaxID=120731;  
 RX [1]  
 SEQUENCE FROM N.A.  
 RA Cranfill R., Kato M.;  
 RT "Phylogenetics, Biogeography, and Classification of the woodwardioid  
 ferns (Blechnaceae)."  
 RRL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.  
 RLL EMBL: AF533866; AAN34645.1; -;  
 RRR Chloroplast.  
 KKW  
 SQ SEQUENCE 185 AA; 20723 MW; D8795983F5283F9E CRC54;  
 Query Match 88.6%; Score 31; DB 8; Length 185;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GRGTP 6  
 I I I I I  
 DB 2 GRGTP 7

RESULT 13  
 Q92K28 PRELIMINARY: PRT: 205 AA.  
 AC Q92K28;  
 DI 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical protein R02299.  
 R02299 GR SMC01349.  
 OS Rhizobium meliloti (*Sinorhizobium meliloti*).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OOC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RX [1]  
 SEQUENCE FROM N.A.  
 RA Capella D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
 RA Bolstad P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
 RA Gadrie T., Goffeau A., Kahn D., Kiss E., Lelaire V., Masuy D.,  
 RA Pohl T., Portetelle D., Pechier A., Furlong R., Ransperger U.,  
 RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;  
 RT "Analysis of the chromosome sequence of the legume symbiont  
*Sinorhizobium meliloti* strain 1021."  
 RLL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 RLL EMBL: AL591790; CAC46878.1; -;  
 KWW Hypothetical protein; Complete proteome.

SQ SEQUENCE 208 AA; 21420 MW; A9222A33301FB522 CRC64;

Query Match 98.6%; Score 31; DB 16; Length 208;

Best Local Similarity 83.3%; Pred. No. 1.8e-02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6

DB 122 GRGDP 127

RESULT 14

Q8N290

ID Q8N290 PRELIMINARY; PRC; 218 AA.

AC Q8N290;

DT 01-OCT-2002 (TRENBLrel. 22, Created);

DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update);

DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update);

DE Hypothetical protein FLJ33651.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;

OC NCBI\_TaxID=9606;

OX 1;

RN SEQUENCE FROM N.A.

RP TISSUE=Amalgam;

RC Ninomiya K., Katsushima M., Kanda K., Kondo H., Yokoi F., Kodaira H.,

RA Furuya T., Takafashi M., Kikawa R., Omura Y., Ake K., Kamihara K.,

RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Ito S.,

RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,

RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,

RA Matsuo K., Nakamura Y., Soxhne M., Kikuchi H., Morakawa K.,

RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,

RA Suzuki Y., Sugano S., Nishihara K., Masuhara Y., Nishii K., Isonai T.,

RT "NEDO human cDNA sequencing project";

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK090970; BAC03560.1;

KW Hypothetical protein.

SQ SEQUENCE 218 AA; 22852 MW; 65468419D52622DF CRC64;

Query Match 86.5%; Score 11; DB 16; Length 218;

Best Local Similarity 83.3%; Pred. No. 1.9e-02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6

DB 4 GRGDP 9

RESULT 15

Q92PA3

ID Q92PA3 PRELIMINARY; PRC; 275 AA.

AC Q92PA3;

DT 01-DEC-2001 (TRENBLrel. 19, Created);

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update);

DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update);

DE Hypothetical protein R01876.

GN R01876 OR SMC00134.

OS Rhizobium meliloti (Sinorhizobium meliloti).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Rhizobiaceae; Sinorhizobium.

OC NCBI\_TaxID=382;

OX 1;

RN SEQUENCE FROM N.A.

RP STRAIN=1021;

RX MEDLINE=21346507; PubMed=1141430;

RA Capela C., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

RA Bolstad P., Becker A., Boutry M., Cadieu F., Dreano S., Gloux S.,

RA Godrie T., Goffeau A., Kahu D., Kiss E., Lelaure V., Masny D.,

RA Pohl I., Portetelle D., Puchler A., Fumele B., Ransperger D.,

RA Renard C., Thebaud P., Vandenbol M., Weidner S., Gallot F.,

RT "Analysis of the chromosome sequence of the legume symbiont

Sinorhizobium meliloti strain 1021";

RL Proc. Natl. Acad. Sci. U.S.A. 98:9677-9682(2001).

DR EMBL; AL591788; CAC46455.1; .

DR InterPro; IPR000051; SAM\_bind.

DR InterPro; IPR001440; TPR.

DR Pfam; PF00515; TPR; 1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 275 AA; 29894 MW; BBE53C168FC340CD CRC64;

Query Match 88.6%; Score 31; DB 16; Length 275;

Best Local Similarity 83.3%; Pred. No. 2.4e-02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRGDP 6

DB 58 GRGDP 63

Search completed: September 16, 2003, 18:17:40

Web time : 35 secs